

OM of: US-09-303-518D-463 to: A_Geneseq_032802:* out_format : pfs
Date: Jun 30, 2002 6:43 AM

About: Results were produced by the GenCore software, version 4.5,
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Command line parameters:

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Search information block:

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Query length: 1887
Database: A_Geneseq_032802:*
Database sequences: 747574
Database length: 111073796
Search time (sec): 627.340000

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seq_documentation_block:

ID AAV38731 standard: Proteoin: 556 AA.

AAV38731:

08-Oct-1999 (first entry)

Neisseria meningitidis strain A antigen encoded by ORF46.

Neisseria meningitidis: Neisseria gonorrhoeae; antigen; vaccine;

treatment: Neisseria infection; meningitis; septicaemia; gonorrhea.

Neisseria meningitidis.

W09924578-A2.

PD 20-MAY-1999.
 XX
 PF 09-OCT-1998; 98MO-IB01665.
 XX
 PR 01-SEP-1998; 98GB-0019016.
 PR 06-NOV-1997; 97GB-0023516.
 PR 14-NOV-1997; 97GB-0024190.
 PR 18-NOV-1997; 97GB-0024386.
 PR 27-NOV-1997; 97GB-0025158.
 PR 10-DEC-1997; 97GB-0026147.
 PR 14-JAN-1998; 98GB-0000759.
 XX
 PA (CHIR-) CHIRON SPA.

PI Grandi G, Masignani V, Pizza M, Rappuoli R, Scarlato V;
 XX WPI. 1999-327407/27.
 DR N-PSDB; AAZ12174.
 XX

Proteins from *Neisseria meningitidis* and *N. gonorrhoeae* useful for
 PT diagnosis, treatment and prevention of infection
 XX

PS Claim 4; Page 277; 524pp; English.

XX Amino acid sequences AAY38499-V38944 represent *Neisseria meningitidis*
 CC and *N. gonorrhoeae* antigenic proteins. They are encoded by open
 CC reading frames (ORFs) AAZ11972-Z12358. The antigenic proteins,
 CC their fragments, their nucleic acids and antibodies are used for
 CC diagnosis, prevention (as vaccines) or treatment of *Neisseria*
 CC infections, such as meningitis, septicemia and gonorrhea. Both
 CC organisms are closely related. Fragments of the nucleic acids
 CC are useful as hybridisation probes and antisense reagents.
 XX

Sequence 556 AA:

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 Ratio: 4.597 Gaps: 8
 Percent Similarity: 85.536 Percent Identity: 77.679

alignment_block:

US-09-303-518D-463 x AAY38731 ..

Align seg 1/1 to: AAY38731 from: 1 to: 556

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17 SleuPromethIleAlaIleHisAlaSerAspLeuAlaAsnAspSerPheIleA 34
101 GCGAGGTCTCGACGCTCAGCATTTGGAACCCGACGGAAATTCACACCTA 150
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34 rgeIlnValIleuAspArgIlnHisPheGluProAspIlyIleuStyIlnIleu 50
151 TTGGGAGAGCGGGGAGGAGCTTGGCCNAGCGACGCGCATGATGGATGGG 200
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201 AAACATACAAAGCCATCAGTTGGGCGACCTGATGATTCACAGGCGCGCG 250
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67 yAsnIleGlnSerHisGlnIleuGlyIlnSerIleuPheIleGlnIlnAlaIle 84
251 TTCAAGGAATATCGGCTACATTCGCTTTTCGATCAGGCGCAAA 300
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84 IeIySglYlnIleGlyIleValIleArgPheSerAspHisGlyIlnIle 100
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134 yGlnHisIleHisProIleAspIlyIleArgIleProGlnIleGlyIlyIle 150
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167 IAlaIleAsnIleIleArgIleAsnIleuThrAspAsnArgSerThrIleGlnIle 184
551 GCGTTGGCGAGCGCTTCCCAATGCGCGCGCTATGCTTACGCAAGAGTA 600
|||||
184 rGleuValAspArgPheHisIleAsnThrIleGlySerMetIleuThrGlnIlyAl 200
601 GCGGACGATTCAAACGCGCCACCGGATACAGCCCGGAGCTTGACAGATC 650
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201 GlyAspGlyPheIlyArgIleAlaThrArgIleSerProGlnIleuAspArgSe 217
651 GCGCAATGCGCGCGGAGGCTTCAACGCGCATGCGATATCGCAAAACA 700
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701 TCATGCGCGCGCGGACGAGAAATGTCGGCGGACGCGATCCGTCAGAGGT 750
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751 ATAGCGAAGGCTCAACATTCGCTGTCATGACGCGCTTGGCTTCGCTTC 800
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251 IleSerGlnGlySerAsnIleAlaIleAlaIleMetIleGlyIleuGlyIleuIleSe 267
801 CACCGAAACAAAGATGCGCGCATCAACGATTTGGCAGATTTGGCGCAAC 850
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851 TCAAAAGACTATGCGCGACGACCATCCGCGATTTGGCGATCCAAACCC 900
|||||
284 eulYAspIlyrAlaIleAlaIleAlaIleArgAspIlyrAlaIleGlnAspPro 300
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951 CCCCATCAAGGGATTTGAGCTGTCCGGGAAATATAGCGCTTTGGCGCGCA 1000
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317 eProValIlySglYIleGlyIleAlaIleValArgGlyIlySglYIleuIlyGlyI 334
1001 TCACGCGCATCTCTGTCAAGCGCTCGCAGATGGCGCGGATTCGCTCCG 1050
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1101 ATACCGCTCCCTTACCATTCGCGAAATATCCGTTCAACTTTGAGCAGC 1150
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367 sTyIleProSerProIyIlnIleSerIleArgAsnIleArgSerAsnIleuIleGlnI 384
1151 CTTCAGGCAAAAGAAACATCAGCTCTCTCAACGCTGCGCGCTCAACGCG 1200
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1201 AAAAATGTCAAACTGGGACGACCAAGCGACCGGAGGAGCGGTACCGGT 1250
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434 rglleAsnThrAlaValProGlnValAsn.....ProIleAsp 446
1345 AACCCGTGTGTGATGCGAAA.....CCGAGATGGGA 1376
447 GluProValPhcAsnProLysSglYserValGlySerAlaHisSerTrpSe 463
1377 GGTGTGATAGACCTTAAT.....AAATTGACACCTCGTGACGAGTGG 1420
463 rIleThraIleArgIleGlnTYrAlaLysLeuProArgGlnGlyArgIleA 480
1421 AG.....AAAAATGTCAGGAACGAGA..... 1443
480 rgtYrIleProProLysAsnTYrSerProSerAlaProLeuProLysGly 496
1443 ..... 1443
497 ProAsnAsnGlyTYrLeuAspLysPhcGlyAsnGlnTYrThrLysGlyPr 513
1444 AGAAGAGTCAGACGAGTCAGTTTAAAGCCATGCGCAA..... 1482
513 oSerArgTYrLysGlyGlnGluPhcGluTYrAspValGlnLeuSerLysT 530
1483 .....CGAGAA.....TGGGAAATATTAACAGCGGTACATTTTAAT 1518
530 hrGlyArgGluGlnLeuGlyTYrAlaSerArgAspGlyLysHisLeuAsn 546
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seq_documentation block:

ID AAU27597 standard: Protein; 672 AA.

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XX AC AAU27597;
XX DT 18-DEC-2001 (first entry)
XX DE Neisseria meningitidis fusion protein ORF46.1-741.
XX KW Neisseria gonorrhoeae; leader peptide; fusion protein; ORF46.1;
XX KW Neisseria protein.
XX OS Neisseria meningitidis.
XX OS Synthetic.
XX PN WO200164922-A2.
XX PD 07-SEP-2001.
XX PF 28-FEB-2001; 2001WO-1B00452.
XX PR 28-FEB-2000; 2000GB-0004695.
XX PR 13-NOV-2000; 2000GB-0027675.
XX PA (CHIR-) CHIRON SPA.
XX PI Arico MB, Comanducci M, Galeotti C, Masignani V, Gulliani MM;
XX PI Pizsa M;
XX WPI: 2001-582163/65.
XX DR N-PSDB; AAS43894.
XX PT Producing heterologous proteins from Neisseria meningitidis and N.
XX gonorrhoeae -

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PS Example 23; Page 64; 119pp; English.
XX
CC The invention relates to methods for the heterologous expression of
CC Neisseria proteins from Neisseria meningitidis and Neisseria
CC gonorrhoeae. At least one domain in the protein is deleted, e.g. the
CC leader peptide, and may be replaced by a domain from a different protein
CC to make a fusion protein, in order to enhance heterologous expression of
CC Neisseria proteins. Also, a region of a protein, such as a poly-glycine
CC stretch, can be mutated to enhance expression. The proteins used in the
CC processes include ORF46.1, 287, 741, 919, 953, 961 and 983. Sequences
CC AAU27553-AAU27610 represent Neisseria proteins and peptide regions of
CC proteins of the invention.
XX
SQ Sequence 672 AA;

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alignment_scores:

Quality	Length
2146.00	564
Ratio: 4.443	Gaps: 9
Percent Similarity: 85.638	Percent Identity: 77.128

alignment_block:

US-09-303-518D-463 x AAU27597 ..

Align seg 1/1 to: AAU27597 from: 1 to: 672

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123 TTTTCGACCGCAGGGGAAATACACCTTATTCGGCAGCAGGGGGAGCTTG 172
18 sPhcGluProAspGlyLysTYrHisLeuPhcGlySerArgGlyLeuAs 35
173 CCNACCGCAGCGCCATATCGATTGGGAACATATCAACCATCATCTG 222
35 laGlaArgSerGlyHisIleGlyLeuGlyLysIleGlnSerHisGlnLeu 51
223 GGCACCTGATGATTCACACAGCGCGCTTGAAGGAATATCGGTACAT 272
52 GlyAsnLeuMetIleGlnGlnAlaIleLysGlyAsnIleGlyTYrI 68
273 TGTCCGCTTTTCCGATCACGGGCGACAAATTCATCGCCTTCGACAAAC 322
68 eValAlaArgPheSerAspHisGlyHisGluValHisSerProPheAsn 85
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85 laIaSerHisSerAspSerAspGluIaGlySerProValAspLysPhe 101
373 AGCCCTTACCGCATCCATTGGAGGAGATACGAACCATCCCGCGAGCG 422
102 SerLeuTYrArgIleHisIleIleIleIleIleIleIleIleIleIle 118
423 CTATGACGGGCCACAGGGCGGCGCTATCCGCTCCAAAGCGCGAGG 472
118 YTYrAspGlyProGlnGlyGlyTYrProAlaProLysGlyAlaArgA 135
473 ATATATACAGCTACGACATAAAGCGGTTGCCCAAATATCCGCTACAC 522
135 spIleTYrSerTYrAspIleLysGlyValAlaGlnAsnIleArgLeuAsn 151
523 CTGACCGACAGCAGCGACGCGACAGCGGCTTGGCGACCGTTTCACAA 572
152 LeuThrAspAsnArgSerThrGlyAlaArgLeuAlaAspArgPheHisAs 168
573 TCACCGCGCTATGTCGACCAAGAGTAGCGCAGCATTCAAACCGCGCA 622
168 naIleGlySerMetLeuThrGlnGlyValGlyAspLysPheLysArgAlaT 185
623 CCCGATACAGCCCGAGCTGAGACAGATGGGCAATCCCGCGCAACCTTC 672
185 hrArgTYrSerProGluLeuAspArgSerGlyAsnAlaIleGlnAlaPhe

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alignment_block:
us-09-303-518d-463 x AAE10032 ..

Align seg 1/1 to: AAE10032 from: 1 to: 672

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2 SerAspLeuAlaAsnSerPheIleArgIleValLeuAspArgIleIln 18
123 TTTCGAACCCGACGGGAAATACCACTATTCGGCAGCAGGGGGAGACTTG 172
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   |||||
18 sPheGluProAspGlyLysThrHisLeuPheGlySerArgGlyGluLeuA 35
173 CCNAGCCCAACGGCCATATCGATTGGGAAACATACAAACCCATCGATTG 222
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   |||||
   |||||
35 laGluArgSerGlyHisIleGlyLeuGlyLysIleGlnSerHisGlnLeu 51
223 GGCACCTGATGATTCACAGCGCGCGTGAAGAAATATCGCTACAT 272
   |||||
   |||||
   |||||
52 GlYAsnLeuMetIleGlnIleAlaIleIleGlyAsnIleGlyTril 68
273 TGTCGGCTTTCCGATCAGCGGCACAAATTCATTGCCCTTGACACACC 322
   |||||
   |||||
   |||||
68 eValArgPheSerAspHisGlyHisGlyValHisSerProPheAspAsn 85
323 ATGCTTCACATTCGGATTCTGACGAAGCGGTAGTCCCGTTGACGGAATT 372
   |||||
   |||||
   |||||
85 lAlaSerHisSerAspSerAspGluAlaGlySerProValAspGlyPhe 101
373 AGGCTTACCGCATTCATTGGAGGATACGAACACCATCCCGCCGACGG 422
   |||||
   |||||
   |||||
102 SerLeuThrArgIleHisThrAspGlyLysGlnHisIleProAlaAspG 118
423 CTATGACGGCCACAGGGCGCGCTATCCGCTCCCAAGCGCGACGG 472
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   |||||
118 YTrAspGlyProGlnGlyGlyLysProAlaProLysGlyAlaArgA 135
473 ATATATACAGCTACGACATTAAGCGGTTCCCAAAATATCCGCTCAC 522
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   |||||
135 splIeTrSerTrAspIleLysGlyAlaAlaGlnHisIleArgLeuAsn 151
523 CTGACCGCAACCGCAGCACCGGACAAACGGTTCGCCAGCTTTCACAA 572
   |||||
   |||||
   |||||
152 LeuThrAspAsnArgSerThrGlyGlnArgLeuAlaAspArgPheHisA 168
573 TGCGGGCGCTATGCTGACCGCAAGAGATGAGCGCAGATTCAACGGCCA 622
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168 nAlaGlySerMetLeuThrGlnGlyValGlyAspGlyPheLysArgAla 185
623 CCCGATACAGCCCGGAGCTGGACAGATCGGCAATGCGCGCAAGCCTTC 672
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185 hTrArgTrSerProGluLeuAspArgSerGlyAsnAlaAlaGluAlaPhe 201
673 AACGGCAGTCAGATATCGTCAAAAACATCATCGCGCGCGCAGAGAAAT 722
   |||||
   |||||
   |||||
202 AsnGlyThrAlaAspIleValLysAsnIleIleGlyAlaAlaGlyIle 218
723 TGTCGGCGCAGCGGATCCCTGACGGGTATACCGAAAGGTCAAACTTG 772
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   |||||
   |||||
218 eValGlyAlaGlyAspAlaValGlnGlyLysSerGlnGlySerAsnIleA 235
773 CTGTCATGACAGCGCTGGGTCTGCTTTCACGCAAAAACAGATGGCGCG 822
   |||||
   |||||
   |||||
235 lAlaValMetHisGlyLeuGlyLeuLeuSerThrLysAsnLysMetAlaArg 251
823 ATCAACGATTTGGCAGATATGCGCAACTCAAAAGACTATGCGCCAGCAGC 872
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252 lLeAsnAspLeuAlaAspMetAlaGlnLeuLysAspTrpAlaAlaAla 268
873 CATCCGGGATTTGGGCACTCCAAAACCCCAATGCCGCAACAGGATAGAAG 922
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268 alLeArgAspTrpAlaValGlnAsnProAsnAlaAlaGlnGlyIleGluA 285

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923 CCGTCAGCAATATCTTTATGGCAGCCATCCCATCAAGAGGATTGAGCT 972
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973 GTCCGGGGGAAATACGCTTTGGCGGCATCAACGGCAGACTCTGTCAAGCG 1022
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   |||||
302 ValArgGlyLysTrpGlyLeuGlyGlyIleThrAlaHisProIleLysAr 318
1023 GTCGAGATGGGCGGATCGCATTCGGCAAGGAAATCCGCGTCAGCG 1072
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   |||||
   |||||
318 gSerIleMetGlyAlaIleAlaLeuProLysGlyLysSerAlaValSerA 335
1073 ACAATTTTCCGATCGCGCATATCGCAAAATACCCGCTCCCTTACCATTC 1122
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   |||||
335 sPAsnProPheAlaAspAlaAlaTrpAlaLysTrpProSerProTrpHisSer 351
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   |||||
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352 ArgAsnIleArgSerAsnLeuGlnGlnArgTrpGlyLysGluAsnIleTh 368
1173 CTCCCAACCCGTCGCGCGCTCAAAACGGCAAAATGTCAAACTGGCAGACC 1222
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   |||||
368 lSerSerThrValProProSerAsnGlyLysAsnValLysLeuAlaAspG 385
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385 lNArgHisProLysThrGlyAlaProPheAspGlyLysGlyPheProAsn 401
1273 TTTGAGAACGACGTGAAATATGATACGAAGCTCGATATTCAGAAATTATC 1322
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402 PheGluLysHisValLysTrpAspThrGly.....Se 412
1323 GGGGGCGGTATACCTAAGCT.....AAGCTGTGTTATGTCG. 1362
   |||||
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   |||||
412 rGlyGlyGlyGlyAlaAlaAlaAspIleGlyAlaGlyLeuAlaAspAla 429
1363 .....AAACCGAGATGGAGGTTGATAGGAAGCTTAATAATTGCAACT 1407
   |||||
   |||||
   |||||
429 eUThrAlaProLeuAspHisLysAspLysGlyLeuGlnSerLeuThrLeu 445
1408 CGTGACAGAGGTGGAGAAATGTTTCAGAAACGACAGACAGAGTCAGAG 1457
   |||||
   |||||
   |||||
446 AspGlnSerValArgLysAsn...GluLysLeuLysLeuAlaAlaGlnG 461
1458 TTAGTCAGTTAAAGCCCATGCGCAACGAGAAATGGGAAATTAACAGGCT 1507
   |||||
   |||||
   |||||
461 yAlaGlu...LysTrpTrpGlyAsnGlyAspSerLeuAsnThrGlyLys 477
1508 TAGATTTTAATCATTTTATAGGTGATATCAATTAAGAAAGCACACTA 1557
   |||||
   |||||
   |||||
477 eUlysAsnAspLysValSerArgPheAspPheIleArgGlnIleGluVal 493
1558 ACAGAGAGG...CAATGCTTAACCCGCTGATGATGACGGGTGATACAA 1604
   |||||
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   |||||
494 AspGlyGlnLeuIleThrLeuGlnSerGlyGluPheGlnValTrpLysG 510
1605 AACCTCGGCACTGATTAACATGAGGGTTTATCAACGG.....ACAGGG 1648
   |||||
   |||||
   |||||
510 nSer.....HisSerAlaLeuThrAlaPheGlnThrGlnG 522
1649 AAATTAATAAAGCCTGATGAAGTTGGAGGTGAAGAAACGAAAAAGT... 1695
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   |||||
   |||||
522 lIleGlnAspSerGlnHisSerGlyLysMetValAlaLysArgIlePhe 538
1696 .....GGGAAAGTATGACACAGCACACCATGTTCCCAAAA 1731
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539 ArgIleGlyAspIleAlaGlyGlnHisThrSerPheAspLys 552

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seq_documentation_block:

ID AAU27599 standard; Protein: 751 AA.
xx

AC AAU27599;
XX
DT 18-DEC-2001 (first entry)
XX
DE Neisseria meningitidis fusion protein ORF46.1-961c.
XX
KW Neisseria gonorrhoeae; leader peptide; fusion protein; ORF46.1;
XX
KW Neisseria protein.
XX
OS Neisseria meningitidis.
XX
OS Synthetic.
XX
PM WO200164922-A2.
XX
PD 07-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-1B00452.
XX
PR 28-FEB-2000; 2000GB-0004695.
XX
PR 13-NOV-2000; 2000GB-0027675.
XX
PA (CHIR-) CHIRON SPA.
XX
PI Arico MB, Comanducci M, Galeotti C, Masignani V, Gulliani MM;
PI Pizza M;
XX
DR WPI: 2001-582163/65.
DR N-PSDB: AAS43896.
XX
PT Producing heterologous proteins from Neisseria meningitidis and N.
PT gonorrhoeae -
XX
PS Example 23; Page 66; 119pp; English.
XX
CC The invention relates to methods for the heterologous expression of
CC Neisseria proteins from Neisseria meningitidis and Neisseria
CC gonorrhoeae. At least one domain in the protein is deleted, e.g. the
CC leader peptide, and may be replaced by a domain from a different protein
CC to make a fusion protein, in order to enhance heterologous expression of
CC Neisseria proteins. Also, a region of a protein, such as a poly-glycine
CC stretch, can be mutated to enhance expression. The proteins used in the
CC processes include ORF46.1, 287, 741, 919, 953, 961 and 983. Sequences
CC AAU27553-AAU27610 represent Neisseria proteins and peptide regions of
CC proteins of the invention.
XX
SQ Sequence 751 AA;

alignment_scores: length: 602
 Quality: 2133.50 Gaps: 7
 Ratio: 4.390 Percent Identity: 72.425
Percent Similarity: 80.731

alignment_block:
US-09-303-518D-463 x AAU27599 ..

Align seg 1/1 to: AAU27599 from: 1 to: 751

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2 SerAspLeuAlaAsnSperPheIleArgIleValLeuAspArgIleHis 18

123 TTTCGAACCCGACGGGAATACACCATTCCTCGACAGCGAGGAGCTTG 172
|||||
18 spHeGluProAspGlyLysTyrHisLeuPheGlySerArgGlyGluLeuA 35

173 CCNAGCGCACGGCCATATCGATTGGGAAACATACAAAGCCATCAGTTG 222
|||
35 IeGluArgSerGlyHisIleGlyLeuGlyLysIleGlnSerHisGlnLeu 51

223 GGGCAGCTGATGATTCACACAGGCGCGTGAAGGAAATATCGGCTACT 272
|||||
52 GlyAsnLeuMetIleGlnIleAlaIleAlaIleLysGlyAsnIleGlyTyrI 68

273 TGCCGCTTTTCGATTCACGGGCAAAATTCATTCGCGCTTCGACAAAC 322
|||||
68 eValArgPheSerAspHisGlyHisGlyValHisSerProPheAspHis 85

323 ATGCCATCATTCCGATTCTGACGAAGCCGCTAGTCCGTTGACGATTC 372
|||||
85 IAlaSerHisSerAspSerAspGlnAlaGlySerProValAspGlyPhe 101

373 AGCCTTACCGCATTCATTTGGAGCGGATACGAACCATCCCGCGCAGG 422
|||||
102 SerLeuTyrArgIleHisTyrPaspGlyTyrGlnHisProlAspGly 118

423 CTATGACGGGCGCACAGGCGGCGCTATCCGCTCCCAAGCGCGAGG 472
|||||
118 YTyrAspGlyProGlnGlyGlyTyrProAlaProlGlyLysAlaArgA 135

473 ATATATACAGCTACGACATAAAGCGCTTGCCAAATATCCGCTCAAC 522
|||||
135 spIleTyrSerTyrAspIleLysGlyValAlaGlnAsnIleArgLeuAsn 151

523 CTGACCGACCAACCGGACGACGCAACAGGCTTGCCGCGCTTCACAA 572
|||||
152 LeuTrpAspAsnArgSerThrGlyGlnArgLeuAlaAspArgPheHisAs 168

573 TGCCGCGCTATGCTGACGCAAGAGTAGCGGACGATTCACACGCGCA 622
|||||
168 nAlaGlySerMetLeuThrGlnGlyValGlyAspGlyPheLysArgAlaT 185

623 CCCGATACAGCCCGAGCTGGACAGATCGGGCAATGCCCGCAAGCTTC 672
|||||
185 hrArgTyrSerProGlnLeuAspArgSerGlyAsnAlaIleGlnAlaPhe 201

673 AAGGCACTGCAGATATGCTCAAAACATCATCGGCGCGGAGGAGAAAT 722
|||||
202 AsnGlyTrpAlaAspIleValLysAsnIleIleGlyAlaAlaGlyGluI 218

723 TGTCGGCGCAGCGCATGCGCTGACGGGTATTAAGCAGAGGCTCAAACTTG 772
|||||
218 eValGlyAlaGlyAspAlaValGlnGlyIleSerGlnGlySerAsnIleA 235

773 CTGTATCAGCAGCGCTGGGTGCTGCTTTCACCGCAAAACAGATGGCGC 822
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235 IAlaMetHisGlyLeuGlyLeuLeuSerThrGlnAsnLysMetAlaArg 251

823 ATCAACGATTTGGCAATATGGCGCAACTCAAGACTATCGCGGAGCAGC 872
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873 CATCCGCGATTGGGCGAGTCCAAAACCCCAATCGCGCACAGGCTAGAG 922
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268 aIleArgAspTrpAlaValAlaGlnAsnProAsnAlaAlaGlnGlyIleGluA 285

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285 IAlaIleSerAsnIlePheMetAlaIleIleProlIleGlyIleGlyAla 301

973 GTCCGGGGAATAATACGGCTTGCGCGCATCAAGCGCATCTGTCAAGCG 1022
|||||
302 ValArgGlyLysTyrGlyLeuGlyGlyIleThrAlaHisProlIleLysAr 318

1023 GTCCGAGATGGGCGCGATTCGATTCGCGAAGGGAATTCGCGCTCAGCG 1072
|||||
318 gSerGlnMetCylAlaIleAlaIleAlaLeuProlGlyLysSerAlaValSerA 335

1073 ACAATTTTGGCGATGCGGATACGCCAAATACCGCTTCATCATTC 1122
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335 spAsnPheAlaAspAlaAlaTyrAlaLysTyrProSerProTyrHisSer 351

1123 CGAATATCCGTTCAAACTTGAGCAGCGCTTAAGGCAAAAGAAACATCAC 1172
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352 ArgAsnIleArgSerAsnLeuGlnArgTyrGlyLysGlnAsnIleThr 368

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1173 CTCCTCAACCGTCCGCGCTCAACGCAAAATGTAACATGGACACC 1222
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1223 AACGCCACCCGAAGACAGCGCTACCGTTGACGGTAAGGGTTCCGAA 1272
1224 |||||
385 InArgHisProLysThrGlyValProPheAspGlyLysGlyPheProAsn 401
1273 TTTCGAGACAGCGTGAATATGATACGACGTCGATATTCAGAAATTATC 1322
1274 |||||
402 PheGlyLysHisValLysThrAspThrGly.....Se 412
1323 GGGGGCGGTATATACCTTAAGCGTCTGTTGATGCGAAACCGAGAT 1372
1324 |||||
412 rGlyGlyGly..... 415
1373 GGGAGGTGATGAGAGCTTAATTAATTGACAACTCGTGACGAGTGGAG 1422
1374 |||||
416 .....GlyAlaThrAsnAspAspValLys 424
1423 AAAAATGTCAGGAACGAGAGAGAGTCAAGTACAGTCACTTAAAGC 1472
1424 |||||
425 LysAlaAlaThrValAlaIleAlaAlaIleTyraAsn..... 437
1473 CCATGCGCAACGAGAAATGGGAAATTAACAGGGTTAGATTAAATCAT 1522
1474 |||||
438 .....GlyGlnGlnIleAsnGlyP 444
1523 TTATAGCTGCT.....GATATCAATTAAGAGCCACAGTACAA 1560
1524 |||||
444 heLysAlaGlyGlnThrIleTyraAspIleAspGlnAspGlyThrIleThr 460
1561 GGAGGCGCATCTACCCGTTGGTGTATGACGGGTGATCAACAAACCC 1610
1612 |||||
461 ...LysLysAspAlaThrAlaAlaAspValGluAlaAspAspPheLysG 476
1611 GGCACCTGATTAACATGGGGTTTATCAACGACGATGGAATTAATAAC 1660
1612 |||||
476 yLeuGlyLeuLysValValThrAsnLeuThrLysThrValAsnGluA 493
1661 CTGATGGAAGTTGGAGGTGAAACGAAAGGAGGAGGAGGAGGAGGAG 1710
1662 |||||
493 snLysGlnAsnValAspAlaLysValLysAlaLysIleSerGlnIleGlu 509
1711 AACGACACCATGTTCCCAAAAGATGGAGCTAGAGTAAATTAGGCTGA 1760
1712 |||||
510 LysLeuThrThrLysLeuAlaAspThrAspAlaAla.....LeuAlaAs 524
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1811 AGGGTACAGTAATCGGGTATTAATAATGAGAGATTTACCGACCTAAT 1860
1812 |||||
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1861 AGAACA 1866
551 LysThr 552
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seq_documentation_block:
ID AAE10034 standard; Protein: 751 AA.
XX
AC AAE10034;
XX
DT 29-NOV-2001 (first entry)
XX
DE N. meningitidis strain 2996 ORF46.1-961c fusion protein.
XX
KW Heterologous expression: Neisserial protein; open reading frame; ORF;
KW ORF46.1-961c fusion protein.

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XX
OS Neisseria meningitidis 2996.
XX
PN WO200164920-A2.
XX
PD 07-SEP-2001.
XX
PE 28-FEB-2001; 2001WO-IB00420.
XX
PR 28-FEB-2000; 2000GB-0004695.
XX
PR 13-NOV-2000; 2000GB-0027675.
XX
PA (CHIR-) CHIRON SPA.
XX
PI Arico MB, Comanducci M, Galeotti C, Maignani V, Giuliani MM;
PI Pizza M;
XX
DR WPI; 2001-557776/62.
XX
DR N-PSDB; AAD17049.
XX
PT Heterologous expression for the expression of two or more Neisserial
PT proteins in fused state
XX
PS Claim 18; Page 26; 52pp; English.
XX
CC The present invention relates to a method for simultaneous heterologous
CC expression of two or more Neisserial proteins which are in a fused
CC state. The method is useful for simultaneous heterologous expression of
CC two or more Neisserial proteins. A protein that may be unstable or
CC poorly expressed on its own is assisted by adding a suitable hybrid
CC partner and commercial manufacture is simplified- only one expression and
CC purification need to be employed in order to produce two separately-
CC useful proteins. The present sequence is Neisseria meningitidis
CC (serogroup B, strain 2996) ORF46.1 (open reading frame)-961c fusion
CC protein.
XX
SQ Sequence 751 AA;
XX
alignment_scores:
Quality: 2133.50 Length: 602
Ratio: 4.390 Gaps: 7
Percent Similarity: 80.731 Percent Identity: 72.425
alignment_block:
US-09-303-518D-463 x AAE10034 ..
Align seg 1/1 to: AAE10034 from: 1 to: 751
73 TCAGATTGGCAACGATCCCTTATCCGCGAGGTTCTCGACCGTCAGCA 122
74 |||||
2 SerAspLeuAlaAsnAspSerPheIleArgGlnValLeuAspArgGlnI 18
123 TTTCGACCCGACGGGAATACACACTTATGCGGACGAGGGGAGCTTG 172
124 |||||
18 sPheGlnProAspGlyLysTyrHisLysLeuPheGlySerArgGlyLysLeuA 35
173 CCNAGCCGACGGCCATATCGGATGGGAATCAATCAAAAGCCATCAGT 222
174 |||||
35 IagIuArgSerGlyHisIleGlyLeuGlyLysIleGlnSerHisGlnLeu 51
223 GGCACCATGATGATCAACAGCGCGCGCTTAAAGAAATATCGGCTACAT 272
224 |||||
52 GlyAsnLeuMetIleGlnGlnAlaIleLysGlyAsnIleGlyTyrI 68
273 TGTCCGCTTTTCGATCAAGGGCACAATTCATTCGCTTCGACAAAC 322
274 |||||
68 eValArgPheSerAspHisGlyHisGlyValHisSerProPheAspAsn 85
323 AMGCTCACATTCCGATTCGACGAAGCGGTAGTCCGCTGACGAGTTC 372
324 |||||
85 IAlaSerHisSerAspSerAspGluAlaGlySerProValAspGlyPhe 101

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373 AGCCTTTACCGCATTCATTGGAGCAGATACGAACACCATCCGCGCAGCG 422
 102 SerLeuTyrTrpGlnHisTrpAspGlyTyrGlnHisProAlaAspGln 118
 423 CTATGACGGGCGCACAGGGGGCGGTATCCGCTCCCAAGCGCGCAGGG 472
 118 YTrpAspGlyProGlnGlyGlyTyrProAlaProLysGlyAlaArgA 135
 473 ATATATACAGCTACGACATAAAGCGCTTGCCTCAAAATATCCGCTCAAC 522
 135 spLeuTyrSerTyrAspIleuGlyValAlaGlnHisnIleArgLeuAsn 151
 523 CTGACGACACACCGCAGACACCGGACAGCGCTTCCGACGCTTTCACAA 572
 152 LeuThrAspAsnArgSerThrGlyGlnArgLeuAlaAspArgPheHisAs 168
 573 TGGCGGCGCATGCTGACGCAAGAGATAGCGCATTCGATCAACGCGCA 622
 168 nAlaGlySerMetLeuThrGlnGlyValGlyAspGlyPheLysArgAlaT 185
 623 CCCGATACAGCCCCGAGCTGACAGATCGGCAATCGCGCAGCGCTTC 672
 185 hTrpArgTyrSerProGluLeuAspArgSerGlyAsnAlaAlaGlnAlaPhe 201
 673 AACGGCACTGCGAGATATCGTCAAAACATCATCGCGCGCGCAGAGAAAT 722
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 218 eValGlyAlaGlyAspAlaValAlaGlnGlyIleSerGlnGlySerAsnIleA 235
 773 CTGTCTACGACGCGCTTGGCTCTCTTCCACCGAAACAGATGGCGCGC 822
 235 lValMetHisGlyLeuGlyLeuLeuSerThrGlnAsnLysMetAlaArg 251
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 923 CCGTCAGCAATATCTTTATGGCAGCCATCCCATCAAAAGGATGGAGCT 972
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 1023 GTTCGAGATGGCGCGCATGTCGCAAGGAAAGAAATCCGCGTCAGCG 1072
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 1073 ACAATTTTCCGATGGCGCATACGCCAAATACCGCTCCCTTACCATTC 1122
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 1173 CTCTCTAACCGTCCGCGCTCAAAACGGCAAAATGTCAAACTGGAGAGC 1222
 368 rSerSerThrValProProSerAsnGlyLysAsnValLysLeuAlaAspG 385
 1223 AACGCCACCGAAGACAGCGCTACCGTTTGGACGTTAAAGGCTTCCGAT 1272
 385 lArgHisProLysThrGlyValProPheAspGlyLysGlyPheProAsn 401
 1273 TTTGAGAACGACGTAATATGATACGAAGCTCGATATTCAAGAAATTATC 1322

402 PheGlnLysHisValLysTyrAspThrGly.....Se 412
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 412 rGlyGlyGly..... 415
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 461 ..LysLysAspAlaThrAlaAlaAspValGlnAlaAspAspPheLysG 476
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 1661 CTGATGAGAGTTGGAGGTGAAACGAAAGAGGTGGAAAGTGATGACC 1710
 493 snLysGlnAsnValAspAlaLysValLysAlaAlaGlnUserGlnIleGlu 509
 1711 AAGCACACCATGTTCCCAAAAGATGGATGAGCGCTGAATTAAGCGCTGA 1760
 510 LysLeuThrThrLysLeuAlaAspThrAspAlaAla.....LeuAlaAs 524
 1761 AGTTACTTGGCGCTGGGAAAGTACAAATATGCTTAAGCATTAATAATGGC 1810
 524 PThrAspAlaAla.....LeuAspAlaThrThrA 534
 1811 AGGTACAGATTAATCGGATTAATAATAAGAGATTTACCGAACCTAAT 1860
 534 snAlaLeuAsnLysLeuGlyGlnAsnIleThrThrPheAlaGlnGluThr 550
 1861 AGAACCA 1866
 551 LysThr 552
 seq_name: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:AAU27598
 seq_documentation_block:
 ID AAU27598 standard; Protein; 806 AA.
 XX AAU27598;
 AC
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Neisseria meningitidis fusion protein ORF46.1-961.
 XX
 KW Neisseria gonorrhoeae; leader peptide; fusion protein; ORF46.1;
 KW Neisserial protein.
 XX
 OS Neisseria meningitidis.
 OS Synthetic.
 XX
 PN WO200164922-A2.
 XX
 PD 07-SEP-2001.
 XX
 PF 28-FEB-2001; 2001WO-IB00452.

XX 28-FEB-2000; 2000GB-0004695.
PR 13-NOV-2000; 2000GB-0027675.
XX
XX
XX (CHIR-) CHIRON SPA.
XX
XX Arico MB, Comanducci M, Galeotti C, Massignani V, Guilianni MM;
PI Pizze M;
XX
XX MPI: 2001-582163/65.
DR N-PSDB; AAS43895.
XX
XX Producing heterologous proteins from *Neisseria meningitidis* and *N.*
PT gonorrhoeae -
XX
XX Example 23; Page 65; 119pp; English.
PS
XX The invention relates to methods for the heterologous expression of
CC Neisserial proteins from *Neisseria meningitidis* and *Neisseria*
CC gonorrhoeae. At least one domain in the protein is deleted, e.g. the
CC leader peptide, and may be replaced by a domain from a different protein
CC to make a fusion protein. In order to enhance heterologous expression of
CC Neisserial proteins. Also, a region of a protein, such as a poly-glycine
CC stretch, can be mutated to enhance expression. The proteins used in the
CC processes include ORF4.1, 287, 741, 919, 953, 961 and 983. Sequences
CC AAU27553-AAU27610 represent *Neisseria* proteins and peptide regions of
CC proteins of the invention.
XX
XX Sequence 806 AA:

alignment_scores:
Quality: 2133.50 Length: 602
Ratio: 4.390 Gaps: 7
Percent Similarity: 80.731 Percent Identity: 72.425

alignment_block:

US-09-303-518D-463 x AAU27598 ..

Align seg 1/1 to: AAU27598 from: 1 to: 806

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2 SerAspLeuAlaAsnSerPheIleArgIleValLeuAspArgIle 18
123 TTTCGACCCGAGCGGAAATACCACTATTCGCGAGCGGGAGCTTG 172
|||||
18 sPheGluProAspLeuLysTyrHisLeuPheGlySerArgGlyLeu 35
173 CCNAGCCGAACGGCCATATCGATTGGGAACATACAAAGCCATCAGTTG 222
|||
35 laGluArgSerGlyHisIleGlyLeuGlyLysIleGlnSerHisGlnLeu 51
223 GGGCACTGATGATTAACAGCGCGCGTTGAAGAAATATCGGCTACAT 272
|||||
52 GlYAsnLeuMetIleGlnGlnAlaIleLeuGlyAsnIleGlyTyrI 68
273 TGTCGGCTTTTCGATCAGCGGACAAATTCATTCGCGCTTGACAAAC 322
|||||
68 eValArgPheSerAspHisGlyHisGluValHisSerProPheAsp 85
323 ATGGCTACATTCGATTCGACAGACCGGTAGTCCGTTGACGATTC 372
|||||
85 lsaIleSerHisSerAspSerAspLeuAlaGlySerProValAspGlyPhe 101
373 AGCTTTACCGCATTCATGGAGAGGATACGAACACCATCCGCGCAGG 422
|||||
102 SerLeuTyrArgIleHisTyrAspGlyTyrGlnHisHisProAlaAspG 118
423 CTATGAGGGCGGACAGGGCGGCTATCCCGTCCCAAGGGCGGAGG 472
|||||
118 yTyrAspLeuProGlnGlyGlyTyrProAlaProLysGlyAlaArg 135

473 ATATATACAGCTACGACATAAAGCGTTGCCAAATATTCGCGCTAC 522
|||||
135 sPleTyrSerTyrAspIleLysGlyValAlaGlnAsnIleArgLeuAsn 151
523 CTGACCGAACAACCGGACGCGGACAAAGCGTTCCGACCTTCCACAA 572
|||||
152 LeuTyrAspAsnArgSerThrGlyGlnArgLeuAlaAspArgPheHis 168
573 TGCCGCGCTATGCTGACGCAAGAGTAGGCGAGGATTCAAAGCGCA 622
|||||
168 nAlaGlySerMetLeuThrGlnGlyValGlyAspGlyPheLysArgAla 185
623 CCCGATACAGCCCCGAGCTGACAGATCGGCAATCCCGCGAAGCTTC 672
|||||
185 hrArgTyrSerProGluLeuAspArgSerGlyAsnAlaAlaGluAlaPhe 201
673 AACGCACTGCGAGATATGCTCAAAAACATCATCGCGCGCGAGAGAAAT 722
|||||
202 AsnGlyThrAlaAspIleValLysAsnIleIleGlyAlaAlaGlyGlu 218
723 TGTCGCGGAGCGGATGCGCGTACAGGTATTAAGCGAAGCTCAAAAT 772
|||||
218 eValGlyAlaGlyAspAlaValGlnGlyIleSerGluGlySerAsnIle 235
773 CTGTCATGACAGCGCTGGGTCTGCTTTCACCGAAACAGATGGCGCG 822
|||||
235 laValMetHisGlyLeuGlyLeuLeuSerThrGluAsnLysMetAlaArg 251
823 ATCAACGATTTGGCAGATATGGCGCACTCAAAAGCTATGCGCGACG 872
|||||
252 lLeAsnAspLeuAlaAspMetAlaGlnLeuLysAspTyrAlaAlaAla 268
873 CATCCGCGATTGGCAGTCACAAACCCCAATGCCGCAAGGCAATGAG 922
|||||
268 alLeArgAspTyrAlaValGlnAsnProAsnAlaIleGlnGlyLeuAla 285
923 CCGTCAGCAATATCTTTATGGCAGCCATCCCATCAAGGATTTGAGCT 972
|||||
285 laValSerAsnIlePheMetAlaAlaIleProIleLysGlyIleGlyAla 301
973 GTCCGGGGAAATACGGCTTGCGGCGCATCACGGCATCTGTCAGACG 1022
|||||
302 vaIArgGlyLysTyrGlyLeuGlyGlyIleThrAlaHisProIleLysAr 318
1023 GTCCGAGATGGCGGCGATGCGATTGCCAAAGGAAATCCGCGTCAGC 1072
|||||
318 gSerGlnMetGlyAlaIleAlaLeuProLysGlyLysSerAlaValSer 335
1073 ACAATTTTGGCGATGCGGATACGCCAAATACCGCTCCCTTACCATTC 1122
|||||
1123 CGAATATTCGTTCAAACTTGAGCAGCGCTTACGGCAAAAGAAATAC 1172
|||||
352 ArgAsnIleArgSerAsnLeuGlnArgTyrGlyLysGluAsnIleThr 368
1173 CTCCTCAACCGTGCAGCGCTCAAAAGCGCAAAATATGCAAGCTGAGAC 1222
|||||
368 rSerSerThrValProProSerAsnGlyLysAsnValLysLeuAlaAsp 385
1223 AACGCCACCGCAAGACAGCGTACCGTTGACGATTAAGGGTTTCGAT 1272
|||||
385 lArgHisProLysThrGlyValProPheAspGlyLysGlyPheProAsn 401
1273 TTTCGAGACACGTAATATATGATACGAAGCTCGATTTCAAGATTTTC 1322
|||||
402 PheGluLysHisValLysTyrAspThrGly.....Se 412
1323 GGGGGCGGCTATACCTAAAGCTATGCTGTTGATGAGAAACGAGAT 1372
|||||
412 rGlyGlyGly..... 415
1373 GGGAGGTGATAGAAAGCTTAATAATTGACAACTCGTGAGCAGGTGAG 1422


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|||||.....|||||.....|||||.....
168 nalaGlySerMetLeuThrGlnGlyValGlyAspGlyPheLysArgAlaT 185
623 CCCGATACAGCCCCGAGCTGGACAGATCGGCGCAATGCGCCGCAAGCTTC 672
|||||.....|||||.....|||||.....
185 hmrGlySerProGlnLeuAspArgSerGlyAsnAlaGluAlaPhe 201
673 AACGGCAGCTGCAGATATGTCAAAAACATCATGCGCGCGCAGAGAAAT 722
|||||.....|||||.....|||||.....
202 AsnGlyThrAlaAspIleValLysAsnIleIleGlyAlaIleGlyIuI 218
723 TGTCCGGCGGCGGATGCCGTGAGGCTATACGGAAGCTCAACATTG 772
|||||.....|||||.....|||||.....
218 eValGlyAlaGlyAspAlaValGlnGlyIleSerGlnGlySerAsnIleA 235
773 CTGTCAATGCAGCGCTTGCTGCTCTTCCACCGAAAAACAAGATGGCGCG 822
|||||.....|||||.....|||||.....
235 lavalMetHisGlyLeuGlyLeuLeuSerThrGlnAsnLysMetAlaArg 251
823 ATCAACGATTGGCAGATATGGCGCAACTCAAGACTATGCCGACAGC 872
|||||.....|||||.....|||||.....
252 IleAsnAspLeuAlaAspMetAlaGlnLeuLysAspTyrAlaIleAla 268
873 CATCCGGATGGGCGAGTCCAAACCCCAATGCCGCAAGGCTATGAAG 922
|||||.....|||||.....|||||.....
268 aIleArgAspTyrAlaValGlnAsnProAsnAlaGlnGlyIleGlnA 285
923 CCGTCAGCAATATCTTTATGGCGAGCCATCCCATCAAGGATGGAGCT 972
|||||.....|||||.....|||||.....
285 lavalSerAsnIlePheMetAlaIleIleProIleLysGlyIleGlyAla 301
973 GTCCGGGGAATATCGGCTTGGGCGCATCACGCAATCTGTCAAGCG 1022
|||||.....|||||.....|||||.....
302 ValArgGlyLysTyrGlyLeuGlyGlyIleThrAlaHisProIleLysAr 318
1023 GTGGCAGATGGGCGCGATGCGATGCCGGAAGGAAATCCCGCTAGCG 1072
|||||.....|||||.....|||||.....
318 gSerGlnMetGlyAlaIleAlaLeuProLysGlyLysSerAlaValSerA 335
1073 ACAATTTGGCGATGGCGCATACGCCAAATACCCGCTCCATACCTTCC 1122
|||||.....|||||.....|||||.....
335 sphaSerPheAlaAspAlaIleTyrAlaLysTyrProSerProLysHisSer 351
1123 CGAAATATCCGTTCAACTTGGAGCAGCGTTACGGCAAGAAACATCAC 1172
|||||.....|||||.....|||||.....
352 ArgAsnIleArgSerAsnLeuGlnArgTyrGlyLysGlnAsnIleTh 368
1173 CTCCCTAACCGTGGCGCGCTCAACGCGCAAAATGTCAACTGGCAGACC 1222
|||||.....|||||.....|||||.....
368 rSerSerThrValProProSerAsnGlyLysAsnValLysLeuAlaAspG 385
1223 AACGCCACCGAAGACAGCGGCTACGCTTGACGCTAAAGGTTCCGAT 1272
|||||.....|||||.....|||||.....
385 lmrGlnHisProLysThrGlyValProPheAspGlyLysGlyPheProAsn 401
1273 TTTGAGAACGACGTAATATGATACGAAGCTCGATATTTCAAGATTATC 1322
|||||.....|||||.....|||||.....
402 PheGlnLysHisValLysTyrAspThrGly.....Se 412
1323 GGGGGCGCGTATATACCTTAAGGCTAGCGCTGTGTTGATCGAAACGAGAT 1372
|||||.....|||||.....|||||.....
412 rGlyGlyGly..... 415
1373 GGGAGCGTTATAGAGCTTAATTAATTGACAACCTGTCAGCAGGTGAG 1422
|||||.....|||||.....|||||.....
416 .....GlyAlaThrAsnAspAspValLys 424
1423 AAAAATGTTCAAGAAACGAAAGAGAGCTCAGAGTAGTCACTTTAAAC 1472
|||||.....|||||.....|||||.....
425 LysAlaIleThrValAlaIleAlaIleAlaIleTyrAsnAsn..... 437
1473 CCATGGCAACGAGATGGGAAATTAACAGGTTAGTTTAAATCAT 1522
|||||.....|||||.....|||||.....

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438 .....GlyGlnGluIleAsnGlyP 444
1523 TTATAGTGT.....GATATCATTAAGAAAGCAGCTACA 1560
|||||.....|||||.....|||||.....
444 heLysAlaGlyGluThrIleTyrAspIleAspGluAspGlyThrIleThr 460
1561 GGAGGCGATAGTCTAACCCGTGTGATGATAGCGTGAATCAACAACTC 1610
|||||.....|||||.....|||||.....
461 ...LysLysAspAlaThrAlaAlaAspValGluAlaAspAspPheLysG 476
1611 GCCACCTGATTAACATGGGCTTTATCAAGCAGACAGTGAATTAAGAGC 1660
|||||.....|||||.....|||||.....
476 LeuGlyLeuLysLysValIleThrAsnLeuThrLysThrValAsnGluA 493
1661 CTGATGGAAAGTGGGAGGTGAACGAAAAAGGCGGAAGTATGATGCC 1710
|||||.....|||||.....|||||.....
493 snLysGlnAsnValAspAlaLysValLysAlaAlaGluSerGluIleL 509
1711 AAGCACACCATGTTCCCAAAAGATTGGGATGAGCTGAGATTAAGGCTGA 1760
|||||.....|||||.....|||||.....
510 LysLeuThrThrLysLeuAlaAspThrAspAlaIle.....LeuAlaAs 524
1761 AGTTACTTCGCTTGGCAAGTACATATATGCTTAAGGATTAATAAGGC 1810
|||||.....|||||.....|||||.....
524 PThrAspAlaIle.....LeuAspAlaThrThrA 534
1811 AGGGTACAAAGTAAATCGGGTATTAATAGAAAGATTACCGAACCTAAT 1860
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534 snAlaLeuAsnLysLeuGlyGlnAsnIleThrThrPheAlaGluGluThr 550
1861 AGACA 1866
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551 LysThr 552

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seq_name: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:AAU27582

seq_documentation_block:

ID AAU27582 standard; Protein; 675 AA.

AC AAU27582;

DT 18-DEC-2001 (first entry)

DE Neisseria meningitidis fusion protein delta-G741-ORP46.1.

KW Neisseria gonorrhoeae; leader peptide; fusion protein; ORP46.1;

KW Neisserial protein.

OS Neisseria meningitidis.

OS Synthetic.

PN W0200164922-A2.

PD 07-SEP-2001.

PF 28-FEB-2001; 2001WO-IB00452.

PR 28-FEB-2000; 2000GB-0004695.

PR 13-NOV-2000; 2000GB-0027675.

PA (CHIR-) CHIRON SPA.

PI Arico MB, Comanducci M, Galeotti C, Mesigiani V, Gulliani MM;

PI Pizza M;

DR WPI; 2001-582163/65.

DR N-PSDB; AAS43881.

PT Producing heterologous proteins from Neisseria meningitidis and N.

PT gonorrhoeae -

PS Example 15; Page 53; 119pp; English.

CC The invention relates to methods for the heterologous expression of
 CC Neisserial proteins from Neisseria meningitidis and Neisseria
 CC gonorrhoeae. At least one domain in the protein is deleted, e.g. the
 CC leader peptide, and may be replaced by a domain from a different protein
 CC to make a fusion protein, in order to enhance heterologous expression of
 CC Neisserial proteins. Also, a region of a protein, such as a poly-glycine
 CC stretch, can be mutated to enhance expression. The proteins used in the
 CC processes include ORF46.1, 287, 741, 919, 953, 961 and 983. Sequences
 CC AAU27553-AAU27610 represent Neisserial proteins and peptide regions of
 CC proteins of the invention.

XX Sequence 675 AA;

alignment_scores:

Quality: 2112.00 Length: 410
 Ratio: 5.189 Gaps: 0
 Percent Similarity: 99.268 Percent Identity: 97.073

alignment_block:

US-09-303-518D-463 x AAU27582 ..

Align seg 1/1 to: AAU27582 from: 1 to: 675

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120 GCATTGTGAACCGCAGCGGAAATACACCTATTCCGAGCAGGGGGAGC 169
   |||||||
274 nHsPheGluProaspGlyLysTyrHisLeuPheGlySerArgGlyLul 291
170 TTGCCNAGCCCAAGCGCCATATCGATTGGGAAACATACAAACCATCAG 219
   |||||
291 euAlaGluArgSerGlyHisIleGlyLeuGlyLysIleGlnSerHisGln 307
220 TTGGGCACTGATGATCAACAGCGCGCGTTGAAGGAATATCGGCTA 269
   |||||
308 LeuGlyAsnLeuMetIleGlnGlnAlaIleLeuGlyAsnIleGlyTyr 324
270 CATGTCCGGCTTTCGATCAGCGGCGCAAAATTCATTCGCGCTCGACA 319
   |||||||
324 rIleValArgPheSerAspHisGlyHisGluValHisSerProPheAsp 341
320 ACCATGCCCTACATTCGATTCGACGAGACCGGTAGTCCCGTTGACGGA 369
   |||||||
341 snHisAlaSerHisSerAspSerAspGlyIleArgLysSerProValAspGly 357
370 TTTCAGCCTTACCGCATCCATTCGAGCGGATAGACACCATCCCGCGCA 419
   |||||||
358 PheSerLeuTyrArgIleHisIleStrAspGlyTyrGluHisIleProAlaAs 374
420 CGGCTATAGCGGCGCAGGCGCGGCTATCCCGCTCCAAAGGCGCGA 469
   |||||||
374 pGlyTyrAspGlyProGlnGlyGlyTyrProAlaProLysGlyAla 391
470 GGGATATATACGCTACGACATAAAGCGCTGCGCAAAATATCCGCTC 519
   |||||||
391 rGAspIleTyrSerTyrAspIleGlyAlaAlaGlnAsnIleArgLeu 407
520 AACCTGACCGACAACCGACGCGCAACGCGCTTCCGACCGTTTCCA 569
   |||||||
408 AsnLeuThrAspAsnArgSerThrGlyGlnArgLeuAlaAspArgPheH 424
570 CAATCGCGGCGCTATGCTGACGCGCAAGAGTAGGAGCGAGTTCAAAACGCG 619
   |||||||
424 sAsnAlaGlySerMetLeuThrGlnGlyValGlyAspGlyPheLysArg 441
620 CCACCGCATACAGCCCGAGCTGACAGATCGGCAATCGCGCGAAGCC 669
   |||||||
441 lathArgTyrSerProGluLeuAspArgSerGlyAsnAlaIleGlyAla 457
670 TTCACGGCAGCTGAGATATCGTCAAAAACATCATCGCGCGGCGAGAGA 719

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|||||
458 PheAsnGlyThrAlaAspIleValLysAsnIleIleGlyAlaIleGly 474
720 AATTTGCGCGCAGCGCATGCGCTGCACAGGTATTAAGCAAGGCTCAACA 769
474 uIleValGlyAlaGlyAspAlaValGlnGlyIleSerIleLysSerAsn 491
770 TTGCTGTATGACGCGCGCTGGCTGCTGCTTTCACCGAAGCAATGAGCG 819
491 lAlaValMetHisGlyLeuGlyLeuLeuSerThrGlnAsnLysMetAla 507
820 CGCATCAACGATTTGGCAGATATGGCGCACTCAAAAGCTATGCGCGACG 869
508 ArgIleAsnAspLeuAlaAspMetAlaGlnLeuLysAspTyrAlaAla 524
870 AGCCATCCGCGCATTTGGCAGTCCAAACCGCAATGCCCGCACAGCATAG 919
524 aAlaIleArgAspTyrAlaValGlnAsnProAsnAlaIleGlnGlyIleG 541
920 AAGCGTCAGCAATATCTTATAGCGAGCCATCCCATCAAGAGGATTGGA 969
541 lAlaValSerAsnIlePheMetAlaIleProIleLysGlyIleGly 557
970 GCTGTCCGGGGAATATACGCGCTTGGCGCGCATACGCGCATCTGTGCA 1019
558 AlaValArgGlyLysTyrGlyLeuGlyIleThrAlaHisProIleLys 574
1020 GCGGTCGAGATGGCGGATGCGCATTCGCGAAGAGAAATCCGCGCTCA 1069
574 sArgSerGlnMetGlyAlaIleAlaLeuProLysGlyLysSerAlaValS 591
1070 GCGACAATTTTCCGATCGCGGATACGCCAAATACCGCTCCCTTACCAT 1119
591 eRAspAsnPheAlaAspAlaIleTyrAlaLysTyrProSerProGlyHis 607
1120 TCCCGAAATATCCGTTCAACTTGGAGCAGCGTTACGGCAAGAAATAT 1169
608 SerArgAsnIleArgSerAsnLeuGlnIleArgTyrGlyLysGluAsnI 624
1170 CACCTCCCTCAACCGTGCAGCGCGCTCAAAACGCGCAAAATGTCAACTGCGAG 1219
624 eThrSerSerThrValProProSerAsnGlyLysAsnValLysLeuAla 641
1220 ACCAAGCGCCAGCAAGACAGCGGTACCGTTGACGCTTAAGAGGTTTCCG 1269
641 spGlnArgHisProLysThrGlyValProPheAspGlyLysGlyPhePro 657
1270 AATTTGAGAACGACGTGAATATGATACG 1299
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seq_name: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:AAE10031

seq_documentation_block:

ID AAE10031 standard; Protein: 675 AA.

XX AAE10031;

AC AAE10031;

AC AAE10031;

DE 29-NOV-2001 (first entry)

DE N. meningitidis strain 2996 delta G741-ORF46.1 fusion protein.

KW Heterologous expression; Neisserial protein; open reading frame; ORF;

KW delta G741-ORF46.1 fusion protein.

OS Neisseria meningitidis 2996.

PN W0200164920-A2.

PD 07-SEP-2001.

PD 28-FEB-2001; 2001WO-IB00420.

PR 28-FEB-2000; 2000GB-0004695.
 PR 13-NOV-2000; 2000GB-0027675.
 XX
 XX (CHIR-) CHIRON SPA.
 PI Arico MB, Comanducci M, Galeotti C, Masignani V, Giuliani MM;
 PI Pizsa M;
 XX
 DR WPI; 2001-557776/62.
 DR N-PSDB; AAD17046.
 XX
 PT Heterologous expression for the expression of two or more Neisserial
 PT proteins in fused state
 PS
 PS Claim 18; Page 22; 52pp: English.
 XX
 CC The present invention relates to a method for simultaneous heterologous
 CC expression of two or more Neisserial proteins which are in a fused
 CC state. The method is useful for simultaneous heterologous expression of
 CC two or more Neisserial proteins. A protein that may be unstable or
 CC poorly expressed on its own is assisted by adding a suitable hybrid
 CC partner and commercial manufacture is simplified-only one expression and
 CC purification need to be employed in order to produce two separately-
 CC useful proteins. The present sequence is Neisseria meningitidis
 CC (serogroup B, strain 2996) delta G741-ORF46.1 (open reading frame)
 CC fusion protein.
 XX
 SO Sequence 675 AA;

alignment_scores:
 Quality: 2112.00 Length: 410
 Ratio: 5.189 Gaps: 0
 Percent Similarity: 99.268 Percent Identity: 97.073.

alignment_block:
 US-09-303-518D-463 x AAE10031 ..

Align seg 1/1 to: AAE10031 from: 1 to: 675

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120 GCATTTCGACCCGACGGAATATACACCATTCGCGACGAGGGGAGC 169
   ::::::::::::::::::::
274 nHisPheGluProAspGlyLysTyrHisLeuPheGlySerArgGlyGlu 291
170 TTGCCNAGCGCAAGCGCATATCGATTGGGAACATACAAAGCATCAG 219
   ::::::::::::::::::::
291 euAlaGluArgSerGlyHisIleGlyLeuGlyLysIleGlnSerHisGln 307
220 TTGGGCGCACTGATGATTCACAGCGCGCGTGAAGGAATTCGGCTA 269
   ::::::::::::::::::::
308 LeuGlyAsnLeuMetIleGlnAlaAlaIleLysGlyAsnIleGlyTyr 324
270 CATTTGCGGCTTTCCGATCAGCGGCAAAATTCATTCGCCCTTGACA 319
   ::::::::::::::::::::
324 rIleValArgPheSerAspHisGlyHisGluValHisSerProPheAsp 341
320 ACATGCGTCACATTCGGATTTCGACGAAGCGGATGCCGTTGACGGA 369
   ::::::::::::::::::::
341 snHisAlaSerHisSerAspSerAspGluValGlySerProValAspGly 357
370 TTGACGCTTACCGCATTCATTTGGAGCGGATAGACACCATCCGCCCA 419
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358 PheSerLeuTyrArgIleHisTyrAspGlyTyrGlnHisProAlaAs 374
420 CGGCTATGACGGGCAACAGCGCGGCTATCCGCTCCCAAGGCGGCA 469
   ::::::::::::::::::::
374 pGlyTyrAspGlyProGlnGlyLysGlyTyrProAlaProLysGlyAla 391
470 GGGATATATACAGCTACGACATAAAGGCGTGGCCAAATATCCGCTC 519
  
```

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391 rGAspIleTyrSerTyrAspIleLysGlyValAlaGlnAsnIleArgLeu 407
520 AACCTGACCGCAACACCGACGACGACGACGACGACGACGACGACG 569
   ::::::::::::::::::::
408 AsnLeuThrAspAsnArgSerThrGlyGlnArgLeuAlaAspArgPhe 424
570 CAATCGCGCGCTATGCTGACGCAAGAGTAGGGACGATTCACAGCG 619
   ::::::::::::::::::::
424 sAsnAlaGlySerMetLeuThrGlnGlyValGlyAspGlyPheLysArg 441
620 CCACCCGATACAGCCCGAGCTGACAGATCGGCGCATCCGCCGAGACC 669
   ::::::::::::::::::::
441 laThrArgTyrSerProGluLeuAspArgSerGlyAsnAlaAlaGluAla 457
670 TTCAACGGCAGTCAGATATGCTCAAAAACATCATCGCGCGGCGAGGA 719
   ::::::::::::::::::::
458 PheAsnGlyThrAlaAspIleValLysAsnIleIleGlyAlaAlaGly 474
720 AATTCGCGCGGCGAGGATGCCGTGACGCTATGAAGCGACGATCAACA 769
   ::::::::::::::::::::
474 uIleValGlyAlaGlyAspAlaValGlnGlyIleSerGluLysSerAsn 491
770 TTGCTGTATGACAGCGCTTGGGCTGCTTCCACCGAAAACAGATGGCG 819
   ::::::::::::::::::::
491 leAlaValMetHisGlyLeuGlyLeuLysSerThrGluAsnLysMetAla 507
820 CGCATCAACGATTTGGCAGATATGGCGCACTCAAAAGCTATGCCGACG 869
   ::::::::::::::::::::
508 ArgIleAsnAspLeuAlaAspMetAlaGlnLeuLysAspTyrAlaAla 524
870 AGCCATCCGCGATTGGCAGTTCACAAACCCCAATGCCCAAGGATAG 919
   ::::::::::::::::::::
524 aAlaIleArgAspTyrAlaValGlnAsnProAsnAlaAlaGlnGlyIle 541
920 AAGCGTCAGCAATATCTTTATGCGAGCCATCCCATCAAGGATTTGA 969
   ::::::::::::::::::::
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   ::::::::::::::::::::
558 AlaValArgGlyLysTyrGlyLeuGlyLysIleThrAlaHisProIle 574
1020 GCGTTCGCGAGATGGCGGATGCGATTCGCAAAAGGAAATCCGCGTCA 1069
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574 sArgSerGlnMetGlyAlaIleAlaLeuProLysGlyLysSerAlaVal 591
1070 GCGACAATTTTGGCGATGCGGATAGCGCAATATCCGCTTACCAT 1119
   ::::::::::::::::::::
591 eArgAspAsnPheAlaAspAlaAlaTyrAlaLysTyrProSerProTyrHis 607
1120 TCCCGCAATATCCGTTCAAACTTGAGCAGCGGTTACGCGCAAGAAACAT 1169
   ::::::::::::::::::::
608 SerArgAsnIleArgSerAsnLeuGlnIleArgTyrGlyLysGluAsnI 624
1170 CACCTCTCAACCGTTCGCGCGGCTCAAAAGGCAAAATGTCAACTGCGAG 1219
   ::::::::::::::::::::
624 eThrSerSerThrValProProSerAsnGlyLysAsnValLysLeuAla 641
1220 ACCAAGCGCCACCGAAGACAGGCGTACCGTTTGACGATTAAGGTTTCG 1269
   ::::::::::::::::::::
641 spGlnArgHisProLysThrGlyValProPheAspGlyLysGlyPhePro 657
1270 AATTTGAGAGCAGCATGAATATGATACG 1299
   ::::::::::::::::::::
658 AsnPheGluLysHisValLysTyrAspThr 667
  
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seq_name: /SIDS1/gcgdata/geneseq/genesep-emb1/AA2001.DAT:AAU27575
 seq_documentation_block:
 ID AAU27575 standard; Protein: 1474 AA.
 XX
 AC AAU27575;

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XX 18-DEC-2001 (first entry)
DT
XX Neisseria meningitidis fusion protein delta-G983-ORF46.1.
DE
XX Neisseria gonorrhoeae: leader peptide: fusion protein; ORF46.1;
KW Neisserial protein.
XX
XX Neisseria meningitidis.
OS Synthetic.
XX
XX MO200164922-A2.
PN
XX
XX 07-SEP-2001.
PD
XX
XX 28-FEB-2001; 2001MO-1B00452.
PF
XX
XX 28-FEB-2000; 2000GB-0004695.
PR 13-NOV-2000; 2000GB-0027675.
XX
XX (CHIR-) CHIRON SPA.
PA
XX
XX Arico MB, Commanducci M, Galeotti C, Masignani V, Gulliani MM;
PI Pizza M;
XX
XX MPI; 2001-582163/65.
DR N-PSDB; AAS43874.
XX
XX Producing heterologous proteins from Neisseria meningitidis and N.
PT gonorrhoeae -
XX
XX Example 15; Page 44; 119pp; English.
XX
XX The invention relates to methods for the heterologous expression of
CC Neisserial proteins from Neisseria meningitidis and Neisseria
CC gonorrhoeae. At least one domain in the protein is deleted, e.g. the
CC leader peptide, and may be replaced by a domain from a different protein
CC to make a fusion protein, in order to enhance heterologous expression of
CC Neisserial proteins. Also, a region of a protein, such as a poly-glycine
CC stretch, can be mutated to enhance expression. The proteins used in the
CC processes include ORF46.1, 287, 741, 919, 953, 961 and 983. Sequences
CC AAU27553-AAU27610 represent Neisserial proteins and peptide regions of
CC proteins of the invention.
XX
XX
SQ Sequence 1474 AA;
XX
XX
XX alignment_scores:
XX Quality: 2112.00 Length: 410
XX Ratio: 5.189 Gaps: 0
XX Percent Similarity: 99.268 Percent Identity: 97.073
XX
XX alignment_block:
XX US-09-303-518D-463 x AAU27575 ..
XX
XX Align seg 1/1 to: AAU27575 from: 1 to: 1474
XX
XX 70 GCCCTCAGATTGGCAAGCATCCCTTATCCGGCAGGTTCTGCACGCTCA 119
XX ::::::::::::::::::::::::::::
XX 1057 SerSerAspLeuAlaAsnAspSerPheIleArgGlnValLeuAspArgG1 1073
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XX 120 GCATTTCGACCCGACGGGAAATACACACTATTTCGACGAGGGGAGC 169
XX ::::::::::::::::::::::::::::::::::::
XX 1073 nHisPheGlnProAspGlyIleArgGlnValLeuPheGlySerArgGlyGln 1090
XX
XX 170 TTGGCCNAGCCCAACGGCATATCGATTGGGAAACATACAAAGCCATCAG 219
XX ::::::::::::::::::::::::::::::::::::
XX 1090 euAlaGlnArgSerGlyHisIleGlyLeuGlyIleGlnSerHisGln 1106
XX
XX 220 TTGGCCACCGTATGATTCACAGCGCGCGCTGACGAAATATCGGCTA 269
XX ::::::::::::::::::::::::::::::::::::
XX 1107 LeuGlyAsnLeuMetIleGlnGlnAlaIleLeuGlyAsnIleGlyTY 1123
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270 CATGTCCGCTTTCCGATCAGCGGACCAAAATTCATTGCGCCTTCGACA 319
XX ::::::::::::::::::::::::::::::::::::
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XX
320 ACCATGCTTCACATTCCTCTGACGAAGCCGGATGCCGTTCGACGGA 369
XX ::::::::::::::::::::::::::::::::::::::
1140 snHisAlaSerHisSerAspSerAspGlnAlaGlySerProValAspGly 1156
XX
370 TTCAGCCTTTACCGCATCCATTCGGACGGATACGAACCAATCCCGCGCA 419
XX ::::::::::::::::::::::::::::::::::::::
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XX
420 CGGCTATGACGGGGCCACAGGGGGCGGCTATCCGCTCCCAAGGCGCA 469
XX ::::::::::::::::::::::::::::::::::::::
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XX
470 GGGATATATACAGCTACGACATAAAGCGTTCGCCAAATATCCGCTC 519
XX ::::::::::::::::::::::::::::::::::::::
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XX
520 AACCTGACCGACACCGGACGACGAGACAGGCTTCGCGACCGTTTCCA 569
XX ::::::::::::::::::::::::::::::::::::::
1207 AsnLeuTHrAspAsnArgSerThrGlnArgLeuAlaAspArgPheHi 1223
XX
570 CAATGCGGCGCTATGCTGACGCAAGAGTAGCGCAGGATTCAAACGCG 619
XX ::::::::::::::::::::::::::::::::::::::
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XX
620 CCACCCGATACAGCCCCGAGCTGGACAGATGGGCAATGCCGCGACGCC 669
XX ::::::::::::::::::::::::::::::::::::::
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XX
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XX ::::::::::::::::::::::::::::::::::::::
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XX
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XX ::::::::::::::::::::::::::::::::::::::
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XX
820 CGCATCAACGATTTGGCAGATATGCGCAACTCAAAAGCTATGCCGCGAC 869
XX ::::::::::::::::::::::::::::::::::::::
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XX
870 AGCCATCCGCGATTGGGAGTCCAAACCCCAATGCCGACAGGCAATAG 919
XX ::::::::::::::::::::::::::::::::::::::
1323 alaIleIleArgAspTYrPalaIleValaGlnAsnProAsnAlaIaGlnGlyIleG 1340
XX
920 AAGCGCTCAGCAATATCTTTATGGCAGCCATCCCATCAAGGATTTGGA 969
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970 GCTGTCGGGGGAAATACGGCTTGGGGCGGCATCAGCGACATCCGTGCAA 1019
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1020 GCGGTCGCGAGTGGCGGATCGCATTCGCCGAAGGAAATCCGCGCTCA 1069
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1070 GCGACAATTTTCCGATCGCGGCATACGCCAAATACCGCTCCCTTACCAT 1119
XX ::::::::::::::::::::::::::::::::::::::
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1120 TCCGGAATATCCGTTCAAACTTGAGAGCAGGTTTACGCGCAAAAGAAAT 1169
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1170 CACTCTCTCAACCGTGCAGCGCTCAAAAGCGCAAAATGTCAAACTGCGAG 1219
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1423 ethrSerSerThrValProProSerAsnGlyLysAsnValLysLeuAla 1440
1220 ACAAGCCCGCCGAGACAGCGGTACCGTTACCGTAAAGGTTCCG 1269
1440 spGlnAghisProLysThrGlyValProPheAspGlyLysGlyPhePro 1456
1270 AATTTTGAAGACGCTGAATATGATACG 1299
1457 AsnPhelGlySerHisValLysTyrAspThr 1466
seq_name: /SID1/gcgcdata/geneseq/geneseq_emb1/AA2001.DAT:AAE10022
seq_documentation_block:
ID AAE10022 standard; Protein: 1474 AA.
AC AAE10022;
DT 29-NOV-2001 (first entry)
DE N. meningitidis strain 2996 delta G983-ORF46.1 fusion protein.
KW Heterologous expression: Neisserial protein; open reading frame; ORF:
delta G983-ORF46.1 fusion protein.
OS Neisseria meningitidis 2996.
PN MO200164920-A2.
XX 07-SEP-2001.
PD 28-FEB-2001; 2001WO-IB00420.
PE 28-FEB-2000; 2000GB-0004695.
PR 13-NOV-2000; 2000GB-0027675.
XX (CHIR-) CHIRON SPA.
PA Arico MB, Comanducci M, Galeotti C, Maignani V, Giuliani MM;
PI Piza M;
XX WPI: 2001-557776/62.
DR N-PSDB; AADI7039.
XX Heterologous expression for the expression of two or more Neisserial
PT proteins in fused state
PS Claim 18: Page 14-15; 52pp: English.
XX The present invention relates to a method for simultaneous heterologous
CC expression of two or more Neisserial proteins which are in a fused
CC state. The method is useful for simultaneous heterologous expression of
CC two or more Neisserial proteins. A protein that may be unstable or
CC poorly expressed on its own is assisted by adding a suitable hybrid
CC partner and commercial manufacture is simplified-only one expression and
CC purification need to be employed in order to produce two separately-
CC useful proteins. The present sequence is Neisseria meningitidis
CC (serogroup B, strain 2996) delta G983-ORF46.1 (open reading frame)
CC fusion protein.
XX
SQ Sequence 1474 AA:
alignment_scores:
Quality: 2112.00 Length: 410
Ratio: 5.189 Gaps: 0
Percent Similarity: 99.268 Percent Identity: 97.073
alignment_block:
US-09-303-518D-463 x AAE10022 ..
Align seg 1/1 to: AAE10022 from: 1 to: 1474

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1057 SerSerAspLeuAlaAsnAspSerPheThrLeuGlnValLeuAspArgL 1073
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1073 nhisPhelGlyProAspGlyLysTyrHisLeuPheGlySerArgLysLul 1090
170 TTGCGNAGCGCAAGCGCATTCGATTGGCAACATCAAGCCATCAG 219
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1090 euAlaGluArgSerGlyHisIleGlyLeuGlyLysIleGlnSerHisGln 1106
220 TTGGCGCACCTGATGATTCACAGCGCGCTGACAGAAATATCGGCTA 269
|||||
1107 LeuGlyAsnLeuMetIleGlnGlnAlaAlaIleLysGlyAsnIleGlyL 1123
270 CATTCGCGCTTTTCGATCACGGGCGCAAAATTCATTCGCGCTTCGACA 319
|||||
1123 rIleValArgPheSerAspHisGlyHisGluValHisSerProPheAsp 1140
320 ACCATGCTCATTTCGATTCGACAGCGCGGTAGTCCGTTGACGCA 369
|||||
1140 snHisAlaSerHisSerAspSerAspGluAlaGlySerProValAspGly 1156
370 TTCAGCCCTTACCGCATTCATTCGAGGATACGACACCATCCGCGCGCA 419
|||||
1157 PheSerLeuTyrArgIleHisThrAspGlyTyrGlnHisSerProAlaAs 1173
420 CGGCTATGACGGGCGACAGGGGCGGCTATCCGCTCCCAAGCGCGCA 469
|||||
1173 pGlyTyrAspGlyProGlnGlyGlyTyrProAlaProLysGlyAla 1190
470 GGGATATATACGCTACGACATAAAGCGCTGGCCCAATATCCGCTC 519
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1190 rGaspIleTyrSerTyrAspIleLysGlyValAlaGlnAsnIleArgLeu 1206
520 AACCTGACCGCAACCGGACGCGACAGCGCTTCGCGCGCTTCGA 569
|||||
1207 AsnLeuThrAspAsnArgSerThrGlyGlnArgLeuAlaAspArgPheH 1223
570 CAATGCGGCGCTATGCTGACGCAAGGATAGCGGATTCACACCG 619
|||||
1223 sAsnAlaGlySerMetLeuThrGlnGlyValGlyAspGlyPheLysArg 1240
620 CCACCGCATACAGCCCGGACGCTGACAGATGCGGCATGCGCGGAGCC 669
|||||
1240 IeThrArgTyrSerProGlnLeuAspArgSerGlyAsnAlaAlaGluAla 1256
670 TTCACGGGCGCTGAGATATGTCAAAACATCATTCGCGCGGCGAGAGA 719
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1257 PheAsnGlyThrAlaAspIleValLysAsnIleIleGlyAlaAlaGly 1273
720 AATTCGCGCGCGGCGATGCGGCGGATGATGAGGAGGATTCACACA 769
|||||
1273 uIleValGlyAlaGlyAspAlaValGlnGlyIleSerGlnGlySerAsn 1290
770 TTGCTGTCATGACAGCGCTGGGCTGCTTCCTCCACGGAACAGATGCG 819
|||||
1290 IeAlaValMetHisGlyLeuGlyLeuLeuSerThrGlnAsnLysMetAla 1306
820 CGCATCAACGATTTGGCAGATATGCGCAACTCAAGCATATGCGCGAGC 869
|||||
1307 ArgIleAsnAspLeuAlaAspMetAlaGlnLeuLysAspTyrAlaAla 1323
870 AGCCATCCGCGATTTGGGACGTCACAAACCCCAATGCCGACAGCATAG 919
|||||
1323 AlaIleArgAspThrAlaValGlnAsnProAsnAlaAlaGlnGlyIleG 1340
920 AAGCGTTCAGCATATCTTTATGCGACGCAATCCCATCAAGGATTCGA 969
|||||
1340 IuAlaValSerAsnIlePheMetAlaAlaIleProIleLysGlyIleGly 1356
970 GCTGTCCGGGGAATAAGCGCTTGCGGCGCATCAAGCGCATCTGTCA 1019


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773 CTGTATGACAGGGCTTGGTCTGCTTTCCAGCGAAACAGATGGCCGC 822
568 lavalmetHISglYleuGlyLeuLeuSerThcGlusnlyMetalaarg 584
823 ATGAAGATTGGCAGATATGGGCAACTCAAGACTATGCCGACGAC 872
585 lIeAsnAspLeuAlaAspMetalaGlnLeuLysAspTyrAlaAla1 601
873 CATCCGCGATTGGGCGATCCCAAAACCCCAATGCCGACAGGATGAG 922
601 alleatgAspTyrAlaValaGlnAsnProAsnAlaAlaGlnGly1 618
923 CGCTCAGCAATATCTTATGCGACCCATCCCATCAAGGATGGAGCT 972
618 lavalSerAsnIlePheMetalaAlaIleProIleLysGlyIleGly 634
973 GTCCGGGGAATAATAGGCTTGGGCGCATCCGACATCCCTGTCAGG 1022
635 ValArgGlyLysTyrGlyLeuGlyGlyIleThAlaHisProIleLys 651
1023 GTCCGAGATGGCGCGATGCGCATTCGCGAAAGGAAATCCGCGTCA 1072
651 gserGlnMetGlyAlaIleAlaLeuProLysGlyLysSerAlaVal 668
1073 ACAATTTTGGCGATGGCGCATACGCCAAATACCCGTCCTTACCAT 1122
668 spAsnPhelaAspAlaAlaTyrAlaLysTyrProSerProTyrHis 684
1123 CGAAATATCGCTCAAACTTGGAGCGAGCGTTACGCAAGAAACACT 1172
685 ArgAsnIleArgSerAsnLeuGlnArgTyrGlyLysGlnAsnIle 701
1173 CTCTCAACCGTCCGCGCTCAAAACGCAAAATGTCAACTGCGACAG 1222
701 rSerSerThValProProSerAsnGlyLysAsnValLysIleAla 718
1223 AACGCCACCGAGAGACAGCGCTTACCGCTTGAAGGTTTCCGAA 1272
718 lnaArgHisProLysThrGlyValProPheAspGlyLysGlyPhe 734
1273 TTTGAGAGCAGCGTGAATATGATAGC 1299
735 PheGlnLysHisValLysTyrAspThr 743

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seq_documentation_block:
ID AAE10038 standard; Protein: 751 AA.
XX
AC AAE10038;
XX
DT 29-NOV-2001 (first entry)
XX
DE N. meningitidis strain 2996 961c-ORF46.1 fusion protein.
XX
KW Heterologous expression; Neisserial protein; open reading frame; ORF;
KW 961c-ORF46.1 fusion protein.
XX
OS Neisseria meningitidis 2996.
XX
PN W0200164920-A2.
XX
PD 07-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-IB00420.
XX
PR 28-FEB-2000; 2000GB-0004695.
PR 13-NOV-2000; 2000GB-0027675.
XX
PA (CHIR-) CHIRON SPA.
XX
PI Arico MB, Comanducci M, Galeotti C, Maignani V, Giuliani MM;
PI Pizza M;

```

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XX WPI: 2001-557776/62.
DR N-PSDB; AAD17053.
XX
PT Heterologous expression for the expression of two or more Neisserial
XX proteins in fused state
XX
PS Claim 18; Page 30; 52pp; English.
XX
CC The present invention relates to a method for simultaneous heterologous
CC expression of two or more Neisserial proteins which are in a fused
CC state. The method is useful for simultaneous heterologous expression of
CC two or more Neisserial proteins. A protein that may be unstable or
CC poorly expressed on its own is assisted by adding a suitable hybrid
CC partner and commercial manufacture is simplified-only one expression and
CC purification need to be employed in order to produce two separately-
CC useful proteins. The present sequence is Neisseria meningitidis
CC (serogroup B, strain 2996) 961c-ORF46.1 (open reading frame) fusion
CC protein.
XX
SQ Sequence 751 AA;

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alignment_scores:
    Quality: 2111.00      Length: 409
    Ratio: 5.200          Gaps: 0
    Percent Similarity: 99.267      Percent Identity: 97.311

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alignment_block:

US-09-303-518D-463 x AAE10038 ..

Align seg 1/1 to: AAE10038 from: 1 to: 751

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351 spheGlnProAspGlyLysTyrHisLeuPheGlySerArgGlyLeuA 368
173 CCNAGCGACAGCGCATTCGATTTGGGAACATACAAAGCATCAGTTG 222
368 llaGlnArgSerGlyHisIleGlyLeuGlyLysIleGlnSerHisGln 384
223 GGCCACCTGATGATCAACAGCGCGCTGTGAGAAATATCGCTCAT 272
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365 GlyAsnLeuMetIleGlnGlnAlaIleLysGlyAsnIleGlyTyrI 401
273 TGTCCGCTTTCCGATCAAGGGCAAAATTCATTCGCTTCGACAAAC 322
401 eValArgPheSerAspHisGlyHisGlyValHisSerProPheAsn 418
323 ATGCTCAGATTCGATTCAGACAGCGGATGATCCCGTTGACGATTC 372
418 lsaIaSerHisSerAspSerAspGlnIaGlySerProValAspGlyPhe 434
373 AGCCTTACCGCATCCATTGGAGCGATAGACACCATCCGCGGACGG 422
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423 CTATGACGCGCCACAGGCGCGGCTATCCGCTCCCAAGGCGGAGG 472
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 473 yTyrAspGlyProGlnGlyGlyTyrProAlaProLysGlyAlaArg 490
 473 ATATATACAGCTACGACATAAAGGGTTGCCAAATATCCGGCTCAAC 522
 490 SPLeuTyrSerTyrAspIleLysGlyValAlaGlnHisHisLeuAsn 506
 523 CTGACCGCAACACCGCAGCACCAGCAACGGCTTCCGACCGTTCACAA 572
 507 LeuThrAspAsnArgSerThrGlyGlnArgLeuAlaAspArgPheHis 523
 573 TGCCGGCGCTATGCTGACGCAAGGAGTAGCGAGGATTCACACGCGCA 622
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 1223 AAGGCCACCGGAGACAGGCTACCGTTGACGCTAAAGGTTTCCGAA 1272
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1273 TTTCGAGACGACGTCGAATATGATACG 1299
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 AC AAE10041;
 XX
 XX
 DT 29-NOV-2001 (first entry)
 XX
 XX
 DE N. meningitidis strain 2996 961cL-ORF46.1 fusion protein.
 XX
 KW Heterologous expression; Neisserial protein; open reading frame; ORF;
 KM 961cL-ORF46.1 fusion protein.
 XX
 OS Neisseria meningitidis 2996.
 XX
 PN W0200164920-A2.
 XX
 PD 07-SEP-2001.
 PF 28-FEB-2001; 2001WO-IB00420.
 XX
 PR 28-FEB-2000; 2000GB-0004695.
 PR 13-NOV-2000; 2000GB-0027675.
 XX
 PA (CHIR-) CHIRON SPA.
 PI Arico MB, Comanducci M, Galeotti C, Maignani V, Giuliani MM;
 PI Piza M;
 XX
 DR WPI: 2001-557776/62.
 DR N-PSDB: AAD17056.
 XX
 PT Heterologous expression for the expression of two or more Neisserial
 PT proteins in fused state -
 XX
 PS Claim 18; Page 32-33; 52pp; English.
 XX
 CC The present invention relates to a method for simultaneous heterologous
 CC expression of two or more Neisserial proteins which are in a fused
 CC state. The method is useful for simultaneous heterologous expression of
 CC two or more Neisserial proteins. A protein that may be unstable or
 CC poorly expressed on its own is assisted by adding a suitable hybrid
 CC partner and commercial manufacture is simplified-only one expression
 CC purification need to be employed in order to produce two separately-
 CC useful proteins. The present sequence is Neisseria meningitidis
 CC (serogroup B, strain 2996) 961cL-ORF46.1 (open reading frame) fusion
 CC protein.
 XX
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 XX
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 Percent Similarity: 99.267 Percent Identity: 97.311
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 US-09-303-518d-463 x AAE10041 ..
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 123 TTTCGACCGCAGCGGAAATATCACCTATTTGGCAGCAGCGGGAGCTTG 172
 373 sPheGlnProAspGlyLysTyrHisLeuPheGlySerArgGlyGlnLeuA 390

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Quality: 2111.00 Length: 409
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alignment_block:

US-09-303-518D-463 x AAU27600 ..

Align seq 1/1 to: AAU27600 from: 1 to: 806

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173 CCNAGCGCAAGCGCATATCGATTGGGAAACATACAAAGCCATCAGTTG 222
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423 IacGluArgSerGlyHisIleGlyLeuGlyLysIleGlnSerHisGlnLeu 439
223 GGGCACTGATGATTCACACAGCGCGCTTGAAGAAATATCGCGCTACAT 272
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456 eValArgPheSerAspHisGlyHisGlyValHisSerProPheAspAsnH 473
323 ATGCTTCACATTCGATTCGACGAAGCGGATAGTCCGCTGACGATTC 372
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473 IAlaSerHisSerAspSerAspGluAlaGlySerProValAspGlyPhe 489
373 AGCCTTACCGCATTCGATGGGACGAGATACGAACACATCCGCGCAGCG 422
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423 CTATGACGGGCGCACAGGGCGCGCTATCCGCTCCCAAGCGCGAGGG 472
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506 yTyrAspGlyProGlnGlyGlyTyrProAlaProLysGlyAlaArgA 523
473 ATATATACAGCTACGACATATAAGCGCTTGCCCAAAATATCCGCTCAAC 522
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523 spIleTyrSerTyrAspIleLysGlyValAlaGlnAsnIleArgLeuAsn 539
523 CTGACCGACAAACCGCAGACCGGACAAAGGCTTCCGCGCTTCACAA 572
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540 LeuThiAspAsnArgSerThrGlyGlnArgLeuAlaAspArgPheHisAs 556
573 TGCAGGCGGTATGCTGACGCAAGAGTAGCGAGGATCAACAGCGCCA 622
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556 nAlaGlySerMetLeuThrGlnGlyValGlyLysAspGlyPheLysArgAla 573
623 CCCGATACAGCCCCCGAGCTGGACAGATCGCGCAATCGCCGCAAGCTTC 672
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573 hTrArgTyrSerProGluLeuAspArgSerGlyAsnAlaIleGlnAlaPhe 589
673 AACGCGACTGCAGATATCGTCAAAAACATCATCGGCGCGGAGGAAT 722
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723 TGTGGCGCAGAGCGATCCGTCAGGGTATTAAGCGAAGGCTCAACATTTG 772
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773 CTGTCATGACAGGCTTGGCTGCTTCCACCGAAACAAAGTGGCGCGC 822
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623 IAlaValMetHisGlyLeuGlyLeuLeuSerThrGluAsnLysMetAlaArg 639
823 ATCAACGATTTGGCAGATATGGCGCAACTCAAGACTATGCGCGAGCAGC 872
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640 IleAsnAspLeuAlaAspMetAlaGlnLeuLysAspTyrAlaIleAlaAla 656

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873 CATCCGCGATTTGGCAGTCCCAAAACCCCATATCCGCGACAGGATACAG 922
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656 AlIeArgAspTyrPAlaValGlnAsnProAsnAlaIleGlnGlyIleGluA 673
923 CCGTCAGCAATATCTTTATAGCGCCATCCCATCATCAAGAGGATGGAGCT 972
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673 IAlaValSerAsnIlePheMetAlaAlaIleProIleLysGlyIleGlyAla 689
973 GTCCGGGGGAAATACGCTTGGGCGGCATACAGCGACATCTGTCCACG 1022
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706 gSerGlnMetGlyAlaIleAlaLeuProLysGlyLysSerAlaValSerA 723
1073 ACAATTTTGGCGATCGGCATACGCCAAATACCCGCTCCCTTACCATTC 1122
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723 spAsnPheAlaAspAlaIleAlaTyrAlaLysTyrProSerProTyrHisSer 739
1123 CGAAATATCCGTTCAACTTGGAGCAGCGTTACGGCAAAAGAAACATCAC 1172
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1173 CTCCCAACCCGCGCGCGCTCAAAACGGCAAAATGTCAACTGCGCAGAC 1222
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756 rSerSerThrValProProSerAsnGlyLysAsnValLysLeuAlaAspG 773
1223 AACGCCACCCGCAAGACAGCGCTACCGTTGACGGTGAAGGCTTCCGAT 1272
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773 IArgHisProLysThrGlyValProPheAspGlyLysGlyPheProAsn 789
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790 PheGluLysHisValLysTyrAspThr 798
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ID_AAE10035 standard; Protein; 806 AA.
XX
AC AAE10035;
XX
DT 29-NOV-2001 (first entry)
XX
DE N. meningitidis strain 2996 961-ORF46.1 fusion protein.
XX
KW Heterologous expression; Neisserial protein; open reading frame; ORF;
KW 961-ORF46.1 fusion protein.
XX
OS Neisseria meningitidis 2996.
XX
PN WO200164920-A2.
XX
PD 07-SEP-2001.
XX
PF 28-FEB-2001; 2001MO-IB00420.
XX
PR 28-FEB-2000; 2000GB-0004695.
PR 13-NOV-2000; 2000GB-0027675.
XX
PA (CHIR-) CHIRON SPA.
XX
PI Arico MB, Comanducci M, Galeotti C, Masignani V, Giuliani MM,
PI Pizsa M;
XX
WP1; 2001-557776/62.
XX
DR N-PSDB; AAD17050.
XX
PT Heterologous expression for the expression of two or more Neisserial
XX proteins in fused state

```

PS Claim 18; Page 27; 52pp; English.

CC The present invention relates to a method for simultaneous heterologous
CC expression of two or more Neisserial proteins which are in a fused
CC state. The method is useful for simultaneous heterologous expression of
CC two or more Neisserial proteins. A protein that may be unstable or
CC poorly expressed on its own is assisted by adding a suitable hybrid
CC partner and commercial manufacture is simplified-only one expression
CC purification need to be employed in order to produce two separately-
CC useful proteins. The present sequence is *Neisseria meningitidis*
CC (serogroup B, strain 2996) 961-ORF6.1 (open reading frame) fusion
CC protein.

SQ	Sequence	806 AA;
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406 sPheGluProAspGlyIysTyrIleHisLeuPheGlySerArgGlyLeuAla 423
173 CCMGGCCGAACGGGCATATCGGATTGGGAACAATACAAACCCATCGATTG 222
423 IaGluArgSerGlyHisIleGlyLeuGlyIysIleGlnSerHisGlnLeu 439
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273 TGTCGGCTTTCCGATACAGGGGCAAAATTCATCGCCCTTGACAAAC 322
456 eValaIArgPheSerAspHisGlyHisGlyAlaHisSerProPheAspAsn 473
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490 SerLeuTyrArgIleHisTyrAspGlyTyrGlnHisProAlaAspGly 506
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523 sPleIleTyrSerTyrAspIleGlyGlyAlaAlaGlnAsnIleArgLeuAsn 539
523 CTGACCGCAACCGCAGACCGGCAACCGGCTCCGACGCTTGCCACA 572
540 LeuTyrAspAsnAlaGlySerThrGlyGlnArgLeuAlaAspArgPheHisAs 556
573 TGCCGCGCCCTATGCTGACGCAAGAGAGTACGGGACGATTCAAACGGCGCA 622
556 nAlaGlySerMetLeuThrGlnGlyValGlyAspGlyPheLeuArgAlaI 573
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PR 06-NOV-1997: 97GB-0023516.
PR 14-NOV-1997: 97GB-0024190.
PR 18-NOV-1997: 97GB-0024386.
PR 27-NOV-1997: 97GB-0025158.
PR 10-DEC-1997: 97GB-0026147.
PR 14-JAN-1998: 98GB-0000759.
XX
PA (CHIR-) CHIRON SPA.
PI Grandi G, Maignani V, Pizza M, Rappoli R, Scarlato V;
DR WPI, 1999-327407/27.
XX Proteins from *Neisseria meningitidis* and *N. gonorrhoeae* useful for
PT diagnosis, treatment and prevention of infection
XX
PS Claim 4, Page 274, 524pp: English.
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CC Amino acid sequences AA138499-138944 represent *Neisseria meningitidis*
CC and *N. gonorrhoeae* antigenic proteins. They are encoded by open
CC reading frames (ORFs) AA11972-212358. The antigenic proteins,
CC their fragments, their nucleic acids and antibodies are used for
CC diagnosis, prevention (as vaccines) or treatment of *Neisseria*
CC infections, such as meningitis, septicemia and gonorrhea. Both
CC organisms are closely related. Fragments of the nucleic acids
CC are useful as hybridisation probes and antisense reagents.
XX
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806 AAAACAGATGGCGCGCATCAGATTTGGCAGATATGCGCAATCTCAA 855
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17 gLygAlaSpolYAlaHISgInaArgPheGlyArgTYgLYAlaThrcIna 34
856 GACATGCGCGAGCAGCATCCGCGATGGCGAGTCCCAAAACCCCAATGC 905
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34 rGLeuCySArgSerSerHISProArgLeuLysSerProLysProGIncys 50
906 CGCACAAGGATAGAACCCGTCAGCAATATCTTATGCGACCATCCCA 955
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51 ArgThrArgHISArgSerArgGInGInLysLeuTYrGlySerHISProH 67
956 TCAAGAGGATTTGAGCTGTCCGGGAAATACGCTTGGCGGCATCAGC 1005
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67 sGInaArgSPTrpSerCysProGlyLysIleGInLeuGlyArgHISHisG 84
1006 GCACATCCTGCAAGCGGTGCGAGATGGGCGCATGCGATTCGCGAAAG 1055
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84 LysHISerCysArgAlaValAlaAsp**ArgAspArgIleCysGInArg 100
1056 GAAATCGCGCGTCAGCACAATTTTGGCGATGGCGCATACGCCAATACC 1105
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117 o...SerLeuSerIleProLysTYrProLeuLys.LeuGInGInArgTYr 132
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1256 GTAAAGGTTTCCGAATTTTGAGAACGACGTGAAATATGATACGAGCTC 1305
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1356 TGATCGCAACCGCAGATGGAGCTTGATAGCAAGCTTATTAATGACAA 1405
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283 ThrSerAlaProAspLysHISGlyValLeuSerSerAspSerGlyAsn 298
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AC
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DT 08-OCT-1999 (first entry)
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DE *Neisseria meningitidis* antigen encoded by a partial ORF46.
XX
KW *Neisseria meningitidis*; *Neisseria gonorrhoeae*; antigen; vaccine;
KW treatment; *Neisseria* infection; meningitis; septicemia; gonorrhea.
XX
OS *Neisseria meningitidis*.
XX
PN W09924578-A2.
XX
PD 20-MAY-1999.
XX
PF 09-OCT-1998: 98WO-IB01665.
XX
PR 01-SEP-1998: 98GB-0019016.
PR 06-NOV-1997: 97GB-0023516.
PR 14-NOV-1997: 97GB-0024190.
PR 18-NOV-1997: 97GB-0024386.
PR 27-NOV-1997: 97GB-0025158.
PR 10-DEC-1997: 97GB-0026147.
PR 14-JAN-1998: 98GB-0000759.
XX
XX (CHIR-) CHIRON SPA.

XX Grandi G, Masignani V, Pizze M, Rappuoli R, Scarlato V;
 PI WPI: 1999-327407/27.
 XX DR N-PSDB; AA212172.
 XX PT Proteins from *Neisseria meningitidis* and *N. gonorrhoeae* useful for
 PT diagnosis, treatment and prevention of infection
 XX
 PS Claim 4; Page 274; 524pp; English.
 CC Amino acid sequences AA18499-18494 represent *Neisseria meningitidis*
 CC and *N. gonorrhoeae* antigenic proteins. They are encoded by open
 CC reading frames (ORFs) AA211972-212358. The antigenic proteins,
 CC their fragments, their nucleic acids and antibodies are used for
 CC diagnosis, prevention (as vaccines) or treatment of *Neisseria*
 CC infections, such as meningitis, septicaemia and gonorrhoea. Both
 CC organisms are closely related. Fragments of the nucleic acids
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 AC AAY75498;
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 DT 21-MAR-2000 (first entry)
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 DE *Neisseria gonorrhoeae* ORF 730 protein sequence SEQ ID NO:2470.
 XX
 KW *Neisseria meningitidis*; *Neisseria gonorrhoeae*; antigen; vaccine;
 KW antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
 KW antibacterial; gene therapy.
 XX
 OS *Neisseria gonorrhoeae*.
 XX
 PN W09957280-A2.
 XX
 PD 11-NOV-1999.
 XX
 PF 30-APR-1999; 99WO-US09346.
 XX
 PR 01-MAY-1998; 98US-0083758.
 PR 31-JUL-1998; 98US-0094869.
 PR 02-SEP-1998; 98US-0098994.
 PR 02-SEP-1998; 98US-0099062.
 PR 09-OCT-1998; 98US-0103749.
 PR 09-OCT-1998; 98US-0103794.
 PR 09-OCT-1998; 98US-0103796.
 PR 25-FEB-1999; 99US-0121528.
 XX
 PA (CHIR) CHIRON CORP.
 PA (GENO-) INST GENOMIC RES.
 XX
 PI Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;
 PI Petersen J, Pizze M, Rappuoli R, Ratti G, Scarlato E, Scarselli M;
 PI Tettelin H, Venter JC;
 XX
 DR WPI: 2000-062150/05.
 DR N-PSDB; AA254260.
 XX
 PT Novel *Neisseria* polypeptides predicted to be useful antigens for
 PT vaccines and diagnostics
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 PS Claim 2; Page 1181; 1453pp; English.
 XX
 CC AA53015 to AA254536, AA254537 to AA254615, and AAY74253 to AAY75941
 CC represent novel *Neisseria meningitidis* and *N. gonorrhoeae* polynucleotides
 CC and polypeptides. AA254537 to AA254576 and AA254616 to AA25473 represent
 CC PCR primers used in the exemplification of the present invention. The
 CC polypeptides, the polynucleotides, antibodies and compositions of
 CC the invention can be used as vaccines, as diagnostic reagents, and as
 CC immunogenic compositions. The polypeptides can be used in the
 CC manufacture of medicaments for treating or preventing infection due to
 CC *Neisseria* bacteria (e.g. meningitis and septicaemia), to detect the
 CC presence of *Neisseria* bacteria, or to raise antibodies. They may also


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801 CACCGAAAGATGCGCGCATCAGCATTTGGCAGATATGGCGAAC 850
271 oalagIuGlyIlyPheAlaValIleGlyIleuGlySerValAlaGly 288
851 TCMAAGCATGCGCGGAGCGATCCGATGCGAGTCCAAAACCC 900
288 hegluIyAsnThrArgGluAlaValAspArgTyrIleGlnIuAsnPro 304
901 AATGCCGACAAAGCATAGACCGCTCAGCAATATCTTTATGCGCCAT 950
305 AsnAlaIalagIuThrValGluAlaValPheAsnValAlaIalAla... 320
951 CCCCATCAAGGATTTGAGCTGTCCGGGAAATACGCTTGCGCGCA 1000
320 ..... 320
1001 TCACGCGACATCCTGTCAAGCGGTGCGAGATGGCGCGATGCCATTGGCG 1050
321 .....LysValAlaIalysLeuAlaIalysAlaIalysPro 331
1051 AAAGGAAATCCGCGCTAGCAGCAATTTGCCGATGCGCGCATACGCCAA 1100
332 ...GlyIlyAlaIalValSerGlyAspPheAlaAspSerTylIyIy 347
1101 ATACCGTCCCTTACATTTCCGAAATATTCGTTCAAACTTGAGAGC 1150
347 sLeuAlaIeuserAspSerAlaArgGlnIeutyGlnAsnAlaIySTYA 364
1151 GTTACGCGAAAGAAACATCACCTCTCTCAACGTCGCCCGTCAAGAGCG 1200
364 rG.....GluAla 366
1201 AAAAATGTCAAACTGCGAGACCAACGCCAGAGACAGCGTACCGTT 1250
367 LeuAspIleHisTyrGlnAspLeuIleArgArgIyIle..... 379
1251 TGACGTTAAGGTTTCCGAAATTTGAGAACGACGTAATATGATACGA 1300
380 .AspGlySerSer.....LysPheIleAsnG 388
1301 ACCTGATTTTCAAGATTAATTCGGGGGGGTATACCTAAGCTTAAGCT 1350
388 lYArgGlnIleAspAlaValIThrAsnAspAlaLeuIleGlnAlaIyAsn 404
1351 GTGTTTGAATGCGAAACCGAGATGGAGTTGATAGAACTTAATTAAT 1400
405 ThrIleSerAla.....IleAspIlyProIyAsnPhe 416
1401 GACA.....ACTCGAGACAGTGGAGAAAATGTTCAAGAAACGAGAA 1444
416 uAsnGlnIyAsnAlaGlyGlnIleIyAlaIleThrIleGlnAlaIalAsnG 433
1445 GAAGGATGAGAGTAGTACAGT.....AAAGCCATCGCGAA 1482
433 lngInclIyAsnArgAlaGlnPheThrPheIyIyTyrGlyValHisSerGln 449
1483 CGAGAA.....TGGGAAATTAACAGCGTTA 1509
450 ValIySerTyrIleGlnSerIyIyGlyIle 460
seq_name: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:AAU27594

```

```

seq_documentation_block:
ID AAU27594 standard; Protein; 467 AA.
XX
AC AAU27594;
XX
DT 18-DEC-2001 (first entry)
XX
DE Neisseria meningitidis protein 730 sequence.
XX
KW Neisseria gonorrhoeae; leader peptide; fusion protein; ORF46.1;
XX Neisserial protein.
XX
OS Neisseria meningitidis.
XX
PN M0200164922-A2.
XX
PD 07-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-IB00452.
XX
PE 28-FEB-2000; 2000GB-0004695.
XX
PR 13-NOV-2000; 2000GB-0027675.
XX
PA (CHIR-) CHIRON SPA.
XX
PI Arico MB, Comanducci M, Galeotti C, Masignani V, Gulliani MW;
PI Pizsa M;
XX
DR WPI; 2001-582163/65.
XX
PT Producing heterologous proteins from Neisseria meningitidis and N.
PT gonorrhoeae -
XX
PS Claim 41; Page 59-60; 119pp; English.
XX
CC The invention relates to methods for the heterologous expression of
CC Neisserial proteins from Neisseria meningitidis and Neisseria
CC gonorrhoeae. At least one domain in the protein is deleted, e.g. the
CC leader peptide, and may be replaced by a domain from a different protein
CC to make a fusion protein. In order to enhance heterologous expression of
CC Neisserial proteins. Also, a region of a protein, such as a poly-glycine
CC stretch, can be mutated to enhance expression. The proteins used in the
CC processes include ORF46.1, 287, 741, 919, 953, 961 and 983. Sequences
CC AAU27553-AAU27610 represent Neisserial proteins and peptide regions of
CC proteins of the invention.
XX
SQ Sequence 467 AA:

alignment_scores:
Quality: 752.50 Length: 511
Ratio: 2.280 Gaps: 11
Percent Similarity: 64.579 Percent Identity: 34.247

alignment_block:
US-09-303-518D-463 x AAU27594 ..
Align seg 1/1 to: AAU27594 from: 1 to: 467

13 CGCAAAATATCCTATTGTG.....TCCATAGTGGAGTGGCT 53
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
5 ArgArgLeuThrAsnLeuAlaIalAspAlaValAlaIalAlaIalAla 21

54 GCCGATGATGCAACACCCGTCAGATTTGGCAAGAGATCCCTTATCGCG 103
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
21 uIleGlnProAlaLeuAlaIalAspIleuAlaGlnAspProPheIleHra 38

104 AGTTTTCGACCGTCAAGATTTGCAACCCGAGCGAAATACAGATTTG 153
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
38 sPasnAlaGlnArgGlnHisTyrGlnProGlyIyIySTyrGlnHisIyPhe 54

154 GCGAGC...AGGGGAGCTTGGCCAGCGAGCGCATATGCGATGGG 200
|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```



```

1342 GCTAAGCCTGTGTTGATGCGAAACG.....Ag 1370
      ::||| ::|||
405 .....HisIeuPheProGlyLysProGlyLysThrThreProGlnH 419
1371 ATGGAGCTGTATAGAGAGCTTATATGACAACTCGAGACAGTGG 1420
      ::|||
419 sTPSerAla.....SerLysIleThr..... 426
1421 AGAAATGTTTCAGAAACGAGAAAGAGAGTACAGTACAGTTTAA 1470
      ::|||
427 .....HisIuIleSerAlaIleVal 433
1471 GCCCATGCCAGACGAGATGGAAATATAACAGGCTTACATTTATCA 1520
      ::|||
434 ThrSerProLysThrGlnTrpTyrAlaGlnThrGly..... 445
1521 TTTTATAGTGTGTGATTCATATAGAAAGCAGACAGTACAGAGGCA 1570
      ::|||
446 .....ThrGlyGlyLysT 450
1571 GTCATACCCTGGTGTATGTACGGGTATACACAACTCGCACCTGAT 1620
      ::|||
450 YrIleAlaLysGly.....ArgProAlaArgTrpValSerTyrGluThr 464
1621 AAACATGGGCTTTATCAGCGACAGTGGAAATTAAGCCTGATGAAG 1670
      ::|||
465 ArgAspGlyIleArgIleArgThrVal..... 473
1671 TTGGGAGTGTAAGAAAGAGTGGGAAAGTATGACCAACAGCAACCA 1720
      ::|||
474 ..TyrGluProAlaThr.....GlyLysValVal.....ThrA 484
1721 TGTTCCTCA 1728
      ::|||
484 IaphePro 486

seq_name: /SID1/gcdata/geneseq/geneseq-emb1/AA2001.DAT.AU27596
seq_documentation_block:
ID AU27596 standard; Protein: 353 AA.
XX
AC AU27596;
XX
DT 18-DEC-2001 (first entry)
XX
DE Fusion protein 730-C2 containing IS5 insertion sequence.
XX
KW Neisseria gonorrhoeae; leader peptide; fusion protein; ORF46.1;
XX
KW Neisseria meningitidis.
XX
OS Escherichia coli.
XX
PN WO20016922-A2.
XX
PD 07-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-IB00452.
XX
PR 28-FEB-2000; 2000GB-0004695.
XX
PR 13-NOV-2000; 2000GB-0027675.
XX
PA (CHIR-) CHIRON SPA.
XX
PI Arico MB, Comanducci M, Galeotti C, Massignani V, Guillani MM;
PI Piza M;
XX
XX WPI: 2001-582163/65.
XX
XX Producing heterologous proteins from Neisseria meningitidis and N.
XX
XX gonorrhoeae -
XX
XX Example 21; Page 61; 119pp; English.

```

```

XX
CC The invention relates to methods for the heterologous expression of
CC Neisseria meningitidis and Neisseria
CC gonorrhoeae. At least one domain in the protein is deleted, e.g. the
CC leader peptide, and may be replaced by a domain from a different protein
CC to make a fusion protein, in order to enhance heterologous expression of
CC Neisseria proteins. Also, a region of a protein, such as a poly-glycine
CC stretch, can be mutated to enhance expression. The proteins used in the
CC processes include ORF46.1, 287, 741, 919, 953, 961 and 983. Sequences
CC AU27553-AU27610 represent Neisseria proteins and peptide regions of
CC proteins of the invention.
XX
XX Sequence 353 AA:

alignment_scores:
      Quality: 725.50      Length: 370
      Ratio: 2.834      Gaps: 4
Percent Similarity: 69.189      Percent Identity: 40.811

alignment_block:
US-09-303-518D-463 x AU27596 ..

Align seg 1/1 to: AU27596 from: 1 to: 353

73 TCAGATTGGCAAGAGATCCCTTATCCGCGAGGTTCTGCAGCCTCAGCA 122
   ::|||
2 AlaaSPleuAlaGlnAspProPheIleThrAspAsnAlaGlnArgGlnH 18
123 TTTCGACCCGAGGGAATACACACTATTCGGAGC...AGGGGGAGC 169
   ::|||
18 sTyrGluProGlyLysTyrHisLysPheGlyAspProArgGlySerV 35
170 TTGCGMAGCGGACAGCCATATTCGATTTGGAAACATTCAGACATCAG 219
   ::|||
35 aISerAspArgThrGlyLysIleAsnValIleGlnAspTyrThrHisGln 51
220 TTGGGCGACCTGATGATTCACACAGCGCGCTTGAAGAAATATCGGCTA 269
   ::|||
52 MetGlyAsnLeuLeuIleGlnGlnAlaAsnIleAsnGlyThrIleGlyT 68
270 CATGTCCGCTTTCCGATCAGGGGACAAATTCATTCGCCCTTGACA 319
   ::|||
68 rHisThrArgPheSerGlyHisGlyHisGlyHisGlyHisGlyHisGly 85
85 snHisAlaAlaAspSerAlaSerGlnGlyLysGlyAsnValAspGlyGly 101
370 TTGACCTTTACCGCATTCATTCGGAGGATAGCAACACATCCCGCGCA 419
   ::|||
102 PheThrValTyrArgLeuAsnTrpGlnGlyHisGlnHisHisProAlaAs 118
118 PalatyrAspGlyProLysGlyLysAsnTyrProLysProThrGlyAla 135
470 GGGATATATACGCTACGACATAAAGCGTGGCCCAATATCCGCTC 519
   ::|||
135 rGAspGlyTyrThrTyrHisValAsnGlyThrAlaArgSerIleLysLeu 151
520 AACCTGACGCAACGCGACGCGGCGGCTTCCGATCCCAAGCGCTTCA 569
   ::|||
152 AsnProThrAspThrArgSerIleArgGlnArgIleSerAspAsnTyrSe 168
570 CAATGCCGCGCTATGCTGACGCAAGAGTAGCGCAGGATTCAGACGC 619
   ::|||
168 rAsnLeuGlySerAsnPheSerAspArgAlaAspGlnAlaAsnArgLysM 185
620 CCACCCGATACAGCCCGAGCTGACAGATGGGCAATGCCGCGGAGCC 669
   ::|||
185 etPheGlnHisAsnAlaLysLeuAspArgTrpGlyLysSerMetGluPhe 201

```

```
670 TTCACGGCAGCATGATATGTCATAAATCATCGCGCGCAGAGAGA 719
    :::::::::::::: :::: :::: ::::::::::::::
202 ILeasnglyValAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 218
    :::::::::::::: :::: :::: ::::::::::::::
720 AATTGTGGCGCAGCGCATGCGCGTGCAGGGTATAGCGAAGCTCAACA 769
    :::::::::::::: :::: :::: ::::::::::::::
218 uAlaLeuGlyIleGlyAspIleLeuTyrglyThrArgTyAlaIleAsp 235
    :::::::::::::: :::: :::: ::::::::::::::
770 TTGCTGTATCATGACAGCGCTTGGTCTGCTTCCACCCGAAACAAGATG 819
    :::::::::::::: :::: :::: ::::::::::::::
235 yAlaAlaAlaMetArgAsnIleAlaProLeuProAlaGlyLysPheAla 251
    :::::::::::::: :::: :::: ::::::::::::::
820 CGCATCAAGCATTTGGCAGATATGGCCCACTCAAGACTATATGCGCGAG 869
    :::::::::::::: :::: :::: ::::::::::::::
252 ValIleGlyLeuGlySerValAlaAlaGlyPheGlyLysAsnThrArg 268
    :::::::::::::: :::: :::: ::::::::::::::
870 AGCCATCCGGGATTTGGCAGCTCCAAAACCCCAATGGCGCAAGCATAG 919
    :::::::::::::: :::: :::: ::::::::::::::
268 uAlaValAspArgTyrglyIleGlyLysAsnProAlaAlaAlaGlyThr 285
    :::::::::::::: :::: :::: ::::::::::::::
920 AAGCGCTCAGCATATCTTATGCGACGCCATCCCATCAAGGATTTGGA 969
    :::::::::::::: :::: :::: ::::::::::::::
285 IuAlaValAlaPheAsnValAlaAlaAlaAlaAlaAlaAlaAlaAla 294
    :::::::::::::: :::: :::: ::::::::::::::
970 GCTGTCCGGGAAATATACGGCTTGGCGCGCATCAGCATCTGTCA 1019
    :::::::::::::: :::: :::: ::::::::::::::
295 .....Ly 295
    :::::::::::::: :::: :::: ::::::::::::::
1020 GCGGTCCGAGATGGCGCGCATTCGCGTAAAGGAAATCCGCGCTCA 1069
    :::::::::::::: :::: :::: ::::::::::::::
295 sValAlaLysLeuAlaLysAlaAlaLysPro...GlyLysAlaAlaVal 311
    :::::::::::::: :::: :::: ::::::::::::::
1070 GCGCAATTTTGGCGATGCGCATACGCCCAATACCGCTCCCTTACAT 1119
    :::::::::::::: :::: :::: ::::::::::::::
311 erglyAspPheAlaAspSerTyrglyLysLeuAlaLeuSerAspSer 327
    :::::::::::::: :::: :::: ::::::::::::::
1120 TCCGAAATATCCGTTCAAACTTGAGCAGCGT.....TACGGCAAGA 1163
    :::::::::::::: :::: :::: ::::::::::::::
328 AlaArgIleLeuTyrglyAsnAlaLysTyrglyAlaLeuGlyLysVa 344
    :::::::::::::: :::: :::: ::::::::::::::
1164 AAACATCAC 1173
    :::::::::::::: :::: :::: ::::::::::::::
344 IArgIleSer 347
    :::::::::::::: :::: :::: ::::::::::::::
seq_name: /STDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:AAU27595
seq_documentation_block:
ID AAU27595 standard; Protein; 377 AA.
XX
XX AAU27595;
XX
XX AC
XX
XX DT 18-DEC-2001 (first entry)
XX
XX DE Fusion protein 730-CI containing ISI insertion sequence.
XX
XX KM Neisseria gonorrhoeae; leader peptide; fusion protein; ORF46.1;
XX
XX KM Neisserial protein.
XX
XX OS Neisseria meningitidis.
XX
XX OS Escherichia coli.
XX
XX WO200164922-A2.
XX
XX PN
XX PD 07-SEP-2001.
XX
XX PF 28-FEB-2001; 2001WO-IB00452.
XX
XX PR 28-FEB-2000; 2000GB-0004695.
XX
XX PR 13-NOV-2000; 2000GB-0027675.
XX
XX PA (CHIR-) CHIRON SPA.
XX
XX PI Arico MB, Comanducci M, Galeotti C, Masignani V, Giuliani MM;
```

```
PI Pizza M;
XX
XX DR WPI: 2001-582163/65.
XX
XX PT Producing heterologous proteins from Neisseria meningitidis and N.
XX gonorrhoeae -
XX
XX PS Example 21; Page 61; 119pp; English.
XX
XX CC The invention relates to methods for the heterologous expression of
XX CC Neisserial proteins from Neisseria meningitidis and Neisseria
XX CC gonorrhoeae. At least one domain in the protein is deleted, e.g. the
XX CC leader peptide, and may be replaced by a domain from a different protein
XX CC to make a fusion protein, in order to enhance heterologous expression of
XX CC Neisserial proteins. Also, a region of a protein, such as a poly-glycine
XX CC stretch, can be mutated to enhance expression. The proteins used in the
XX CC processes include ORF46.1, 287, 741, 919, 953, 961 and 983. Sequences
XX CC AAU27553-AAU27610 represent Neisserial proteins and peptide regions of
XX CC proteins of the invention.
XX
XX SQ Sequence 377 AA;
XX
XX alignment_scores:
XX Quality: 723.50 Length: 361
XX Ratio: 2.882 Gaps: 3
XX Percent Similarity: 69.529 Percent Identity: 40.997
XX
XX alignment_block:
XX US-09-303-518D-463 x AAU27595 ..
XX
XX Align seg 1/1 to: AAU27595 from: 1 to: 377
XX
XX 73 TCAGATTTGGCAAGATCCCTTATCCGCGAGTTCGACCGTCAGCA 122
XX :::::::::::::: :::: :::: ::::::::::::::
XX 2 AlaAspLeuAlaGlnAspProPheIleThrAspAsnAlaGlnArgGlnH 18
XX :::::::::::::: :::: :::: ::::::::::::::
XX 123 TTTCGACCCGACGGGAAATACACCTATTCGCGAGC...AGGGGGAGAC 169
XX :::::::::::::: :::: :::: ::::::::::::::
XX 18 sTyrglyProGlyGlyLysTyrglyHisLeuPheGlyAspProArgLyserv 35
XX :::::::::::::: :::: :::: ::::::::::::::
XX 170 TTGCCNAGCGCAGCGCATATCGATTTGGAAACATACAAAGCATCAG 219
XX :::::::::::::: :::: :::: ::::::::::::::
XX 35 alSerAspArgThrGlyLysIleAsnValIleGlnAspTyrglyHisGln 51
XX :::::::::::::: :::: :::: ::::::::::::::
XX 220 TTGGCGCCACCTGATGATTCACAGCGCGCGTGAAGAAATATAGGCTA 269
XX :::::::::::::: :::: :::: ::::::::::::::
XX 52 MetGlyAsnLeuIleGlnGlnAlaAsnIleAsnGlyThrIleGlyTy 68
XX :::::::::::::: :::: :::: ::::::::::::::
XX 270 CATTTGCCGCTTTCCGATCAGGGGCAAAATTCATTCGCCCTTGACA 319
XX :::::::::::::: :::: :::: ::::::::::::::
XX 68 rHisThrArgPheSerGlyHisGlyHisGlnGlnHisAlaProPheAsp 85
XX :::::::::::::: :::: :::: ::::::::::::::
XX 320 ACCATGCTCAGATTCGATTCGACGAAGCGGATGTCCTTGACGGA 369
XX :::::::::::::: :::: :::: ::::::::::::::
XX 85 snHisAlaAlaAspSerAlaSerGlnGlyLysValAspArgGly 101
XX :::::::::::::: :::: :::: ::::::::::::::
XX 370 TTACGCTTATCCGATCCATGCGGATAGCAACACATCCGCGCGA 419
XX :::::::::::::: :::: :::: ::::::::::::::
XX 102 PheThrValTyrglyLeuAsnTrpGlyHisGlnHisHisProAlaAs 118
XX :::::::::::::: :::: :::: ::::::::::::::
XX 420 CGGCTATGACGGCGCACAGGGCGCGCTATCCCGCTCCAAAGCGCGCA 469
XX :::::::::::::: :::: :::: ::::::::::::::
XX 118 palatyAspGlyProLysGlyLysAsnTyrglyProLysProLysGlyAla 135
XX :::::::::::::: :::: :::: ::::::::::::::
XX 470 GGGATATATACAGCTACGACATATAAAGCGTTGCCAAATATCCGCTC 519
XX :::::::::::::: :::: :::: ::::::::::::::
XX 135 rGAspGlyTyrglyThrHisValAsnGlyThrAlaArgSerIleLysLeu 151
XX :::::::::::::: :::: :::: ::::::::::::::
XX 520 AACCTGACGACAGCGGACGCGACGCGGATGCGCGCGCTTGCGATTC 569
XX :::::::::::::: :::: :::: ::::::::::::::
XX 152 AsnProThrAspThrArgSerIleArgGlnArgIleSerAspAsnTyse 168
XX :::::::::::::: :::: :::: ::::::::::::::
```

[illegible]

PA (CHIR-) CHIRON SPA.
XX
PI Rappunoli R;
XX
DR WPI: 2000-687543/67.
XX
XX Novel Neisserial protein fragments and their corresponding nucleic
PI acids, useful in the manufacture of medicines for the prevention of
PI Neisserial infection, and in the manufacture of diagnostic reagents -
XX
PS Claim 15; Page 58; 157pp; English.
XX
XX The present peptide is a conserved region of a Neisserial protein.
CC Neisserial proteins containing this sequence, and the nucleic acids
CC that encode such proteins, are useful in the manufacture of medicines
CC for the prevention of Neisserial infection, and in the manufacture of
CC multi-specific diagnostic reagents.
XX
XX Sequence 125 AA;
SQ

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alignment_scores:
  Quality: 668.00      Length: 125
  Ratio: 5.387         Gaps: 0
Percent Similarity: 99.200  Percent Identity: 96.000
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alignment_block:
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US-09-303-518D-463 x AAB37856

Align seg 1/1 to: AAB37856 from: 1 to: 125

205	ATCAAAAGCCATGATGGGGCCACCGATGATTCAACAGGGGCGGTGA	254
206		255
1	lIeInSerIstGInleuGInSneMetIeGInGInAlAlAlAlIeIy	17
255	AGGAATATGCGGTACATTGTCCGCTTTTCCGATCCAGCAGGACAAATTCC	304
17	sgIAsnIleGIIyTyllAlvalArgPheSerAspIstGInSlyInAln	34
305	ATTGGCCCTTGACAAACCAATGGCTCAACATCCGATTCTGAGAGCCGGT	354
34	IstSerProPheAspAsnIstAlSerIstAspSerAspGlnAlaGly	50
355	AGTCCCGTTACAGCATTCAGCCTTTACGCAATCTGGAGCGGATGAGA	404
51	SeerProValAspIyIyHeSerIeIeuIyIyArgIleIstIyAspArgIyIyGII	67
405	ACACSCATCCGCGCGAGCTATGACAGGGGCACAGGGCGCGGCTATCCG	454
67	uHstIstProAlaAspGIIyTyrAspGIIyProGInIyGIIyIyTyrProA	84
455	CTCCCAAGCGCGAGGATATATACAGTACAGATTAAGAGGGCTTCC	504
84	lArPoluYstGIIyAlaIyAspIleIyTyrSeerIyAspIleIySgIyAlaIa	1004
505	CAAAATATCCGCTCAACCTGACAGCAACGCGACAGCAGCAGCAACGCT	554
101	GlnAsnIleArgIeUsnIeUhrAspAsnIyGerThrGInGInAlaGlye	117
555	TGCGGACGGTTTCCAAATGCCGCG	579
117	uAlaAspArgIyPheIstAsnAlaGIIy	125

```
seq_name: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:AAV75400
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seq_documentation_block:
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XX

DT 21-MAR-2000 (first entry)

DE Neisseria gonorrhoeae ORF 686 protein sequence SEQ ID NO:2274

XX Neisseria meningitidis; Neisseria gonorrhoeae; antigen: vaccine;
KW antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;
KW antibacterial; gene therapy.
OS Neisseria gonorrhoeae.
PN W09957280-A2.
PD 11-NOV-1999.
XX 30-APR-1999; 99WO-US09346.
XX 01-MAY-1998; 98US-0083758.
PR 31-JUL-1998; 98US-0094869.
PR 02-SEP-1998; 98US-0098994.
PR 02-SEP-1998; 98US-0099062.
PR 09-OCT-1998; 98US-0103749.
PR 09-OCT-1998; 98US-0103794.
PR 09-OCT-1998; 98US-0103796.
PR 25-FEB-1999; 99US-0121528.
XX (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
XX Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;
PI Petersen J, Piza M, Rappuoli R, Ratti G, Scalato E, Scarselli M;
PI Tettelin H, Venter JC;
XX WPI: 2000-062150/05.
DR N-PSDB; AA254162.
XX
PT Novel Neisserial polypeptides predicted to be useful antigens for
PT vaccines and diagnostics
XX
PS Claim 2; Page 1101; 1453pp; English.
XX
XX AA253015 to AA254536, AA254577 to AA254615, and AAY74253 to AAY75941
CC represent novel Neisseria meningitidis and N. gonorrhoeae polynucleotides
CC and polypeptides. AA254537 to AA254576 and AA254616 to AA255473 represent
CC PCR primers used in the exemplification of the present invention. The
CC polypeptides, the polynucleotides, antibodies and compositions of
CC the invention can be used as vaccines, as diagnostic reagents, and as
CC immunogenic compositions. The polypeptides can be used in the
CC manufacture of medicaments for treating or preventing infection due to
CC Neisserial bacteria (e.g. meningitis and septicemia), to detect the
CC presence of Neisseria bacteria, or to raise antibodies. They may also
CC be used to screen for agonists or antagonists, which may themselves
CC have use as antibacterial agents. The polynucleotides of the invention
CC may also be used in gene therapy protocols.
XX
XX Sequence 131 AA.
SQ
alignment_scores: Length: 131
 Quality: 657.00 Gaps: 0
 Ratio: 5.015
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-09-303-518D-463/rev x AAY75400 ..
Align seg 1/1 to: AAY75400 from: 1 to: 131
723 AATTTCCTGCGCGCGCATGATGTTTGGACGATTCGACGTGCGGT 674
|||||
1 AsnPhesercysargalaaspaspvalpheaspaspillecysseralava 17
673 TGAAGCGTTGGCGCGCATTCGCCGATCTGCGCACTCGGGGCGTATACGG 624
|||||
17 IGIUGLPHedLYglYlleAlaargSerValgInLeugLYAlaValserg 34
623 GTGCGGTTTGAATCGGTGCGCTACTCTTCCTGCGTCAAGCATAGCGCGCG 574

|||||
34 IYGLYAlaPhedgluSerValaIaTYSerLeuArgGlnHisSerAlaGly 50
573 ATTGTGGAACGGGTGCGCAACCCGTTGCCGCTGCTGGGTTCGGGTCA 524
|||||
51 lleValGIuThrValgLYLysProleuSerValaAlaValaValgLYl 67
523 GGTTCAGCGCGATATTTGGGCAAGCGCTTTATGTCTAGCTATATATA 474
|||||
67 nValGIuAlaaspIleleuGLYAsnAlaAlaPhetyValValaValaLYrI 84
473 TCCTTCGCGCCCTTTGGAGCGGATAGCGCGCCCTGTGGCCGTCATA 424
84 leProArgAlaPhedglYsergLYlleAlaAlaAlaLeuTrpProValIle 100
423 GCCGTGCGCGGATGTTGTCGTATCCCTCCCAATGATGGGATTAAGGC 374
|||||
101 AlaValGIYglYmetValaPhetValSerValaPrometAspAlaValLYsAl 117
373 TGAATCCGTCAAGGAGTACCGGCTTCGTCAAGATCGGAATG 331
|||||
117 eGIuSerValaInGLYThrThngLYPheValArgIleGLYmet 131
seq_name: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:AA75402
seq_documentation_block:
ID AAY75402 standard; Protein: 131 AA.
XX
XX AAY75402;
XX
XX 21-MAR-2000 (first entry)
XX
XX Neisseria meningitidis ORF 686 protein sequence SEQ ID NO:2278.
DE
XX
XX Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KW antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;
KW antibacterial; gene therapy.
XX
XX Neisseria meningitidis.
OS
XX W09957280-A2.
XX
XX 11-NOV-1999.
PD
XX 30-APR-1999; 99WO-US09346.
XX
XX 01-MAY-1998; 98US-0083758.
PR 31-JUL-1998; 98US-0094869.
PR 02-SEP-1998; 98US-0098994.
PR 02-SEP-1998; 98US-0099062.
PR 09-OCT-1998; 98US-0103749.
PR 09-OCT-1998; 98US-0103794.
PR 09-OCT-1998; 98US-0103796.
PR 25-FEB-1999; 99US-0121528.
XX
XX (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
XX Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;
PI Petersen J, Piza M, Rappuoli R, Ratti G, Scalato E, Scarselli M;
PI Tettelin H, Venter JC;
XX WPI: 2000-062150/05.
DR N-PSDB; AA254164.
XX
XX Novel Neisserial polypeptides predicted to be useful antigens for
PT vaccines and diagnostics
XX
XX Claim 2; Page 1101-1102; 1453pp; English.
XX
XX AA253015 to AA254536, AA254577 to AA254615, and AAY74253 to AAY75941
CC represent novel Neisseria meningitidis and N. gonorrhoeae polynucleotides
CC and polypeptides. AA254537 to AA254576 and AA255473 represent

PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to *Neisseria* bacteria (e.g. meningitis and septicaemia), to detect the presence of *Neisseria* bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.

Sequence 131 AA:

alignment_scores:

Quality: 636.00 Length: 131
Ratio: 4.892 Gaps: 0
Percent Similarity: 99.237 Percent Identity: 96.183

alignment_block:

US-09-303-518D-463/rev x AAY75402 ..

Align seg 1/1 to: AAY75402 from: 1 to: 131

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723 AATTTCTCTGCGCGCGCGATGATCTTTTGAAGATATCGATGCCGT 674
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1  AsnPheserCysArgAlaAspValPheAspAlpIleCysSerAla 17
673 TGAAGGCTTCGGCGGATGCCGATCTGTCCAGCTCGGGGCTGTATCG 624
      |||||||
17 LguserPheGlyIleAlaArgSerValGlnLeuGlyAlaValSerG 34
623 GTGCGCGCTTTGAATCCGTGCTACTCTGCGTGCAGATGCGCGCGC 574
      |||||||
34 LylAlaPheGlnuserValAlaTySerLeuArgIlnIshThrArgly 50
573 ATTTGGAAGAGGTGCGCAAGCCGTGTCCGGTGTGCGGTGCGTGA 524
      |||||||
51 IleValGlnThrValAspIlePheSerGlyAlaIleValGlyC1 67
523 GGTGAGGCGGATATTTGGGCAAGCCCTTATGTCGATGATGATATA 474
      |||||||
67 nValGlnAlaAspIleLeuGlyAsnAlaPheTyValAlaValAlaTy 84
473 TCCCTGCGCGCTTTGGAGCGGATAGCGCGCGCTGTGCGCGTATA 424
      |||||||
84 LepArgAlaPheGlySerGlyIleAlaIleAlaLeuTrpProValIle 100
423 GCGGTGCGCGGATGCTGTTCGATCCGCCAATGATGCGGTAAAGGC 374
      |||||||
101 AlaValGlyIleValAlaPheValSerValPrometAspAlaValIle 117
373 TGAATCGGTCAAGGAGTACCGGCTTGTGCAATCGGAATG 331
      |||||||
117 agIuserValasnGlyThrThrGlyPheIleArgIleGlyMet 131

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seq.name: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT: AAY75401

seq_documentation_block:

ID AAY75401 standard; Protein: 163 AA.

AC AAY75401;

DT 21-MAR-2000 (first entry)

DE *Neisseria meningitidis* ORF 686 protein sequence SEQ ID NO:2276.

KW *Neisseria meningitidis*; *Neisseria gonorrhoeae*; antigen; vaccine;

KW antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;

XX antibacterial; gene therapy.

XX *Neisseria meningitidis*.

PN W0957280-A2.

XX 11-NOV-1999.

XX 30-APR-1999; 99WO-US09346.

XX 01-MAY-1998; 98US-0083758.

XX 31-JUL-1998; 98US-0094869.

XX 02-SEP-1998; 98US-0098994.

XX 02-SEP-1998; 98US-0099062.

XX 09-OCT-1998; 98US-0103749.

XX 09-OCT-1998; 98US-0103794.

XX 09-OCT-1998; 98US-0103796.

XX 25-FEB-1999; 99US-0121528.

XX (CHIR) CHIRON CORP.

XX (GENO-) INST GENOMIC RES.

XX Fraser C, Galeotti C, Grandi G, Hickey E, Maignani V, Mora M;

XX Petersen J, Piza M, Rappoli R, Ratti G, Scalato E, Scarselli M;

XX Tettelin H, Venter JC;

XX WPI; 2000-062150/05.

XX N-PSDB; AA254163.

XX Claim 2; Page 1101; 1453pp; English.

XX AA253015 to AA254536, AA254577 to AA254615, and AA774253 to AAY75941

XX represent novel *Neisseria meningitidis* and *N. gonorrhoeae* polynucleotides

XX and polypeptides. AA254537 to AA254576 and AA254616 to AA25473 represent

XX PCR primers used in the exemplification of the present invention. The

XX polypeptides, the polynucleotides, antibodies and compositions of

XX the invention can be used as vaccines, as diagnostic reagents, and as

XX immunogenic compositions. The polypeptides can be used in the

XX manufacture of medicaments for treating or preventing infection due to

XX *Neisseria* bacteria (e.g. meningitis and septicaemia), to detect the

XX presence of *Neisseria* bacteria, or to raise antibodies. They may also

XX be used to screen for agonists or antagonists, which may themselves

XX have use as antibacterial agents. The polynucleotides of the invention

XX may also be used in gene therapy protocols.

XX Sequence 163 AA:

alignment_scores:

Quality: 636.00 Length: 137
Ratio: 4.782 Gaps: 0
Percent Similarity: 97.080 Percent Identity: 91.971

alignment_block:

US-09-303-518D-463/rev x AAY75401 ..

Align seg 1/1 to: AAY75401 from: 1 to: 163

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741 GGCATGCGCTGCGCGCGACATTTCTCTGCGCGCGCGATGATGTTTGA 692
      ||| :|||
27 GlyAla*****AsnPheserCysSerAlaAspValPheAs 43
691 CGATATCTGAGTGCCTTGAAGGCTTCGCGCGATGCGCGATGCTGTC 642
      |||||||
43 nAspIleCysSerAlaValGlnGlyPheGlyIleAlaArgSerValG 60
641 AGCTGCGGCTGTATCGGTCGCGCTTGAATCGCTGCTGCTGCTGTC 592
      |||||||
60 InleuGlyAlaValSerGlyIleAlaPheGlnuserValAlaTySerleu 76
591 CGTCAGATAGCGCGCGCGATGTCGAAGCGTGGCAAGCGCTTGTTCGG 542
      |||||||
77 ArgGlnIshThrThrGlyIleValGlnThrValGlyIlePheLeuSerG 93

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53 AsnAlaArgGlySerVal.....LysAsnArgValCysAlaValAlaGlnTh 67
204 CATACAAAGGCATCAGTTGGCCACCTGARG.....ATTCAACAGG 244
67 rPheAspAlaThrAlaValGlyProIleLeuProIleThrHisGluArgT 84
245 CGGCCCTTGAAGAAATATCGCTACATGTCGGCTTTTCGATCCAGCGG 294
84 hrcIyPheGluGlyValIleGlyTYrGluThrHisPheSerGlyHisGly 100
295 CACAAATTCATTCGCCCTTCGACAACATGCTCACAATTCGATTCGA 344
101 HisGluValHisSerProPheAspAsnHisAspSerLysSerThrSerAs 117
345 CGAAGCGCGAGTACGCTTGACGATTCACGCTTACCCCATCCATCGG 394
117 pPheSerGlyGlyValAspGlyGlyPheThrValTYrGlnLeuHisArgT 134
395 ACGGATACGACACATCCCGCGAGCTATGACGCGGCGACAGCGCGCG 444
134 hrcIySerGluIleHisProAlaAspGlyTYrAspGlyProGlnGlyGly 150
445 GGGTATCCCGCTCCCAAGCGCGAGGATATATACAGCTACGACATAAA 494
151 GlyTYrProGluProGlnGlyAlaArgAspIleTYrSerTYrHisIleTy 167
495 AGGCGTTGCCCAATATCCGCTCAAC..... 522
167 sGlyThrSerThrLysThrLysIleAsnThrValProGlnAlaProPheS 184
523 .....CTGACCGACACCGCGACGACGCGACGCGCTTGCGCGAG 561
184 eArSpArgTrpLeuLysGluAsnAlaGlyAlaAlaSerGlyPheLeuSer 200
562 CGTTTCCACATGCCGCGCTATGCTGACGCAAGAGTAGCGCGCATT 611
201 ArgAlaAspGluAlaGlyLysLeuIleTrpGluAsnAspProAspLysAs 217
612 CAACGCGCGCCGAGTACAGCCCGAGCTGACAGATCGGCGCAATGCCG 661
217 nTPArgAlaAsnArgMetAsp.....AspIleArgGlyIleValG 251
662 CCGAAGCGCTCAAGCGGCACTGACAGATGCTCAAAAACATCATCGGCGG 711
231 IInGlyAlaValAsn.....ProHeLeuThrGlyPhe 241
712 GCAGAGAAATTTGTCGGCGCA.....GGCGATCCGTCGACGGGTATAG 755
242 GInGlyValGlyIleGlyAlaIleThrAspSerAlaValSerProValTh 258
756 CGAAGGCTCAACATGCTGTCATGCACGCG.....TTGGGCTGC 796
258 rAspThrAlaAlaGlnGlnIleThrLeuGlnGlyIleAsnAspLeuGlyAsn 275
797 TTTCACACGAAACAAAGATGGCGCATCAAGATTGGCAGATATGGCG 846
275 eueSrProGluAlaGlnLeuAlaAlaAlaSerLeuGlnAspSerAla 291
847 ...CAACTCAAGACTATGCCGCAAGCATCCGCGATTGGCGAGTCCA 893
292 PheAlaValLysAspGlyIleAsnSerAla...ArgGlnTrpAlaAspAl 307
894 AAACCCCAAT.....GCCGCAAAAGCATATGAGGCCG 925
307 aHisProAsnIleThrAlaThrAlaGlnThrAlaLeuAlaValAlaGlu 333
926 TCACCAATATCTTATGCGACGATCCCATCAAGGGATGGAGCTGTC 975
324 AlaAlaGlyThrValTrpArg.....GlyLysLysValGluLeuAs 337
976 CGGGGAAATATAGCGCTTGCGCG.....GCAT 1001
337 nProThrLysTrpAspTrpValLysAsnThrGlyTYrLysLysProAlaA 354

```

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1002 CACGCGACATC.....CTGTCAAGCGGTGCGAGATGG 1033
354 lArGHisMetGlnThrValAspGlyGluMetAlaGlyGlyAsnArgPro 370
1034 GCGCGATCGCATTCGCCAAGAGAAATCCCGCTGACGCGACATTTTGCC 1083
371 ProLysSerIleThrSerGluGlyLysAlaAsnAlaIleThrTYr.... 385
1084 GATGGGCGATACGCCAATATACCGCTCCCTTACCATTCGCCAATATCCG 1133
386 .....ProLysLeuValAsnGlnLeuAsnG 394
1134 TTCAACTTGGAGACGCTTACGCGCAAG 1162
394 lGlnAsnLeuAsnAsnIleAlaAlaGln 403
seq_name: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1199.DAT:AAV38584
seq_documentation_block:
ID AAV38584 standard; Protein; 498 AA.
XX
AC AAV38584;
XX
DT 08-OCT-1999 (first entry)
XX
DE Neisseria gonorrhoeae antigen encoded by ORF29.
XX
KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
treatment; Neisseria infection; meningitis; septicemia; gonorrhea.
XX
OS Neisseria gonorrhoeae.
XX
PN W09924578-A2.
XX
PD 20-MAY-1999.
XX
PE 09-OCT-1998; 98WO-IB01665.
XX
PR 01-SEP-1998; 98GB-0019016.
PR 06-NOV-1997; 97GB-0023516.
PR 14-NOV-1997; 97GB-0024190.
PR 18-NOV-1997; 97GB-0024386.
PR 27-NOV-1997; 97GB-0025158.
PR 10-DEC-1997; 97GB-0026147.
PR 14-JAN-1998; 98GB-0000759.
XX
PA (CHIR-) CHIRON SPA.
XX
PI Grandi G, Masignani V, Pizza M, Rappuoli R, Scarlato V;
XX
DR WPI: 1999-327407/27.
XX
DR N-PSDB; AA212046.
XX
PT Proteins from Neisseria meningitidis and N. gonorrhoeae useful for
PT diagnosis, treatment and prevention of infection
XX
PS Claim 4; Page 146-147; 524pp; English.
XX
CC Amino acid sequences AAV38499-v38944 represent Neisseria meningitidis
CC and N. gonorrhoeae antigenic proteins. They are encoded by open
CC reading frames (ORFs) AA211972-212358. The antigenic proteins,
CC their fragments, their nucleic acids and antibodies are used for
CC diagnosis, prevention (as vaccines) or treatment of Neisseria
CC infections, such as meningitis, septicemia and gonorrhea. Both
CC organisms are closely related. Fragments of the nucleic acids
CC are useful as hybridisation probes and antisense reagents.
XX
SO Sequence 498 AA;

```

```

alignment_scores:
Quality: 452.00      Length: 427

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CC Orfa and Orfb in complexes with the protein p11C are capable of
 CC adhering to human cells.
 CC Products obtained from the DNA are useful in medicaments,
 CC diagnostic compns. and vaccines, esp. for treatment of
 CC Neisseria gonorrhoea and N. meningitidis infections.

XX Sequence 509 AA;

alignment_scores:
 Quality: 450.00 Length: 417
 Ratio: 1.875 Gaps: 18
 Percent Similarity: 57.554 Percent Identity: 32.374

alignment_block:
 US-09-303-518d-463 x AA18786 ..

Align seg 1/1 to: AA18786 from: 1 to: 509

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31 CTGTCCATCTGCGAGTGGCCGCGATGATGACACAGCCGATTT 80
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16 IISerleuLeuGlnIleProIle.....SerHisAlaSerGlyLe 29
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
81 GGCAGACGATCCCTTATCCGAGGTTCTGCACCGTCAGCATTTGAC 130
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
29 u.....AspAlaArgLeuArgAspAspMetGlnAlaLysHis 44
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
131 CCAGAGGGAATATACCACTATTGCGC..AGCAGGGGGAGCTTGC 177
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
44 roGlyGlyLysTyrHisLeuPheGlyAsnAlaArgLysSerVal 58
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
178 CGCAGCGGCATATCGATGGAGAAACATCAAGCCATCAGTTGGCCA 227
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
59 LysAsnArgValAlcysAlaValGlnThrPheAspAlaThrAlaVal 75
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
228 CCGTATG.....ATTCAACAGCGCGCGCTTGAAGAAATATGCGCT 268
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
75 oIleLeuProIleThrHisGlnArgThrGlyPheGlnGlyIleIle 92
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
269 ACATTCGCCCTTTCCGATCAGCGGACAAATTCATTCGCCCTTCGAC 318
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
92 yrgLutThrHisPheSerGlyHisGlyIleValHisSerProPheAsp 108
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
319 AACCATGCTCATATCCGATTCGATTCGAGACCGGATGCTCCGTTGACG 368
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
109 AsnHisAspSerLysSerThrSerAspPheSerGlyLysValAspGly 125
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
369 ATTCAGCCTTTACCGCATTCGATGGAGCGATAGCAACACCATCCGCG 418
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
125 yPheThrValTyrGlnLeuHisArgThrGlySerGlnIleHisProAla 142
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
419 ACGGCTATGACGGGCCACAGGGGGCGGCTATCCCGTCCCAAGCGCG 468
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
142 spGlyTyrAspGlyProGlnGlyLysLysTyrProGlnGlnGlyAla 158
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
469 AGGATATATACAGCTACGACATAAAGGGCTGCCCAATATTCGGCT 518
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
159 ArgAspLysLysSerLysThrHisLysGlyLysThrThrLysThrLys 175
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
519 CAAC.....CTGACCGACAAAC 535
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
175 eAsnThrValProGlnAlaProPheSerAspArgTyrLeuLysGlnAsn 192
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
536 GCACGACCGGACAAAGCGCTGCGCAGCCGTTCCACAAATGCCGCGCATG 585
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
192 LaglyAlaAlaSerGlyPheLeuSerArgAlaAspGlnAlaGlyLysLeu 208
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
586 CTGACGAGAGAGTAGCGGAGCATTCAAACGCGCCACCGCATACAGCCC 635
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
209 IleTyrPheLysAsnAspProAspLysAsnTyrPheArgAlaAsnArgMet 224
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636 CGAGCTGACGATGGGCAATGCCCGCGAAGCCTTCAACGGGACCTGCAG 685
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225 .....AspIleArgGlyIleValGlnGlyAlaValAsn..... 235
686 ATATCGTCAAAAACATCATTCGCGCGGAGGAGAAATTCGCGGCA... 732
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226 .....ProPheLeuThrGlyPheGlnGlyLeuGlyValGlyAlaIle 249
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
733 ...GGCGATGCCGTCAGGATATAGCGAAGCTCA.....AACAT 770
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
250 ThrAspSerAlaValAsnProValThrTyrAlaAlaAlaArgLysThrLe 266
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
771 TCGTCATATGACAGCGCTTGGCTGCTGCTTTCACCGAAAACAGATGCGC 820
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
266 uGlnGlyIleHisAsnLeuGlyAsnLeuSerProGlnGlnGlnLeuAla 283
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
821 GCATCAACGATTTGGCAGATATGCGG...CAATCAAAAGACTATGCGGCA 867
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
283 laAlaSerLeuLeuGlnAspSerAlaPheAlaValLysAspGlyTyrLeu 299
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
868 GCAGCCATCCGATTTGGGAGTCCCAAAACCCCAATGCCGACAGAGCAT 917
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
300 SerAla...ArgGlnTyrAlaAspAlaHisProAsn..... 311
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
918 AGAAGCCGTCAGCAATATCTTATGCGAGCCATCCCATCAAGAGATG 967
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
311 eThrAlaThrAlaGlnThrAlaLeuAlaValAlaGlnAlaAlaGly... 326
968 GAGCTGTCCGGGAAATACGGCTTGGCGGATTCAGCATCAGCAATCCGTG 1017
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
327 .....ThrValTyrPheLysLysValGlnLeuAsn 337
1018 AAGCGGTGCG...AGATGGCGCGCATTCGATTCGCGAAGGAAATCCGC 1064
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
337 nProThrLysTyrAspTyr..... 343
1065 CGTCAGCGCAATTTTCCCGATGCGGCAATACGCAAAATCCGTCCTT 1114
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
344 .....ValLysAsnThrGlyTyrGlnLysProAla 353
1115 ACCATTCGCGAAATATCGGTTCAAACTTGGAGCAGCGTTACGGCAAGA 1164
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
354 AlaArgPro.....MetGlnThrValAspGlyGlnMetAlaGlyLys 367
1165 AACATCACCTCCTCAACCGTGGCGGCTCAAAACGCAAAAATGTCAAC 1213
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
367 sAsnLysProPheLysProSerThrGlnGlnHisSerThrHisSerAsp 383
seq_name: /SIDS1/9cgcdata/geneseq/geneseq-emb1/AA1999.DAT:AA136583
seq_documentation_block:
ID AA136583 standard; Protein: 468 AA.
XX
AC AA136583;
XX
DT 08-OCT-1999 (first entry)
XX
DE Neisseria gonorrhoeae antigen encoded by ORF29.
XX
KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KW treatment; Neisseria infection; meningitis; septicemia; gonorrhea.
XX
OS Neisseria gonorrhoeae.
XX
PN WO9924578-A2.
XX
PD 20-MAY-1999.
XX
PF 09-OCT-1998; 98WO-IB01665.
XX
PR 01-SEP-1998; 98GB-0019016.
PR 06-NOV-1997; 97GB-0023516.
PR 14-NOV-1997; 97GB-0024190.
PR 18-NOV-1997; 97GB-0024386.
PR 27-NOV-1997; 97GB-0025158.

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396 AlaSerAsnGlyAspTyrHisGlyPheProGlnSerValAspAlaPhe 412
1359 TGGGAACGAGATGGAGGTTGATGAGAGCTAATATGACAAAC 1408
412 T..... 412
1409 GTGAGCAGGTGAGAAAAATGTTACGAAACGAAAGAGAGTCAAGT 1458
412 ..... 412
1459 AGTCAGTTAAAGCCATGCGCAGACGAAATGGGAAATAAACAGGTT 1508
413 ..... GluAsnGlyThrVal 418
1509 AGATTTAATCATTATATAGTGTGAT.....ATCATAAGAAAGCA 1552
418 e.....GlnIleValGlyAspAsnIleValArgHisLysLeuT 432
1553 CAGTAACAGGAGGAGCATAGTCTAAACCGTGTGATGTACGGTATCAAA 1602
432 yrlleProGlySerTyrLysGlyLysAspGlyAsnDheGlyTyrIleArg 448
1603 CAACCTCGGCACCTGATTAACATGGCGTTTAT 1635
449 GluAlaAspGlyLysIleAsnHisArgLeuPhe 459
seq_name: /SIDSL/gcgdata/geneseq/geneseq-embL/AA2000.DAT:AAV74709

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seq_documentation_block:

ID AAV74709 standard; Protein; 385 AA.

AAV74709;

21-MAR-2000 (first entry)

Neisseria meningitidis ORF 238 protein sequence SEQ ID NO:892.

Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;

antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;

antibacterial; gene therapy.

Neisseria meningitidis.

WO9957280-A2.

11-NOV-1999.

30-APR-1999; 99WO-US09346.

01-MAY-1998; 98US-0083758.

31-JUL-1998; 98US-0094869.

02-SEP-1998; 98US-0098994.

02-SEP-1998; 98US-0099062.

09-OCT-1998; 98US-0103749.

09-OCT-1998; 98US-0103794.

09-OCT-1998; 98US-0103796.

25-FEB-1999; 99US-0121528.

(CHIR) CHIRON CORP.

(GENO-) INST GENOMIC RES.

Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;

Petersen J, Pizsa M, Rappuoli R, Ratti G, Scalato E, Scarselli M;

Tetclen H, Venter JC;

WPI: 2000-062150/05.

N-PSDB; AA253471.

Novel Neisserial polypeptides predicted to be useful antigens for

PT vaccines and diagnostics

Claim 2; Page 546; 1453pp; English.

CC AA253015 to AA254536, AA254577 to AA254615, and AAV74253 to AAV75941
 CC represent novel *Neisseria meningitidis* and *N. gonorrhoeae* polynucleotides
 CC and polypeptides. AA254537 to AA254576 and AA254616 to AA254673 represent
 CC PCR primers used in the exemplification of the present invention. The
 CC polypeptides, the polynucleotides, antibodies and compositions of
 CC the invention can be used as vaccines, as diagnostic reagents, and as
 CC immunogenic compositions. The polypeptides can be used in the
 CC manufacture of medicaments for treating or preventing infection due to
 CC *Neisseria meningitidis* (e.g. meningitis and septicaemia), to detect the
 CC presence of *Neisseria meningitidis*, or to raise antibodies. They may also
 CC be used to screen for agonists or antagonists, which may themselves
 CC have use as antibacterial agents. The polynucleotides of the invention
 CC may also be used in gene therapy protocols.

XX SQ Sequence 385 AA;

alignment_scores:

Quality: 408.00 Length: 396

Ratio: 1.830 Gaps: 17

Percent Similarity: 56.313 Percent Identity: 31.818

alignment_block:

US-09-303-518D-463 x AAV74709 ..

Align seg 1/1 to: AAV74709 from: 1 to: 385

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31 CTGTGCATATCGCGAGTGTGCTGCGCTGCGATGCGATGCGCGCTGAGATT 80
16 IleSerLeuLeuGlnIleProLe.....SerHisAlaAsnGlyLe 29
81 GGCAACAGATCCCTTATCCGCGAGTTCGACCGTCGACGATTCGACG 130
29 u.....AspAlaArgLeuArgAspAspMetGlnAlaLysHisTyrGluP 44
131 CCGACGGGAATACCATTCCTGCGC...ACGAGGGGAGCCTTGCCNAG 177
44 roGlyGlyLysTyrHisLeuPheGlyAsnAlaArgGlySerVal..... 58
178 CGCACGGCGCATATCGGATGTTGGGAAACATACAAAGCCATGTTGGGCA 227
59 LysAsnArgValTyrAlaValGlnThrPheAspAlaThrAlaValGlyPr 75
228 CCTGATG.....ATTCAACAGCGCGCGCTGAGAGAAATATCGGCT 268
75 oIleLeuProIleThrHisGlyArgThrGlyPheGluGlyIleIleGlyT 92
92 yfGluThrHisPheSerGlyHisGlyHisGluValHisSerProPheAsp 108
319 AACCATGCTCATTCGATTCGATTCGACGACCGGTAAGTCCCGTTGACGG 368
109 AsnHisAspSerLysSerThrSerAspPheSerGlyGlyValAspGlyL 125
369 ATTCAAGCCTTACCGCATTCGATTCGACGACGATACCAACCATCCCGCG 418
125 yPheThrValTyrGlnLeuHisArgThrGlySerGluIleHisProGluA 142
419 ACGGCTATGACGGGCGACAGGGCGGCGGCTATCCCGTCCCAAGAGCGG 468
142 spGlyTyrAspGlyProGlnGlySerAspTyrProProGlyLysIleAla 158
469 AGGATATATACAGCTACGACATAAAGCGCTGCCCAAAATATCCGCT 518
159 ArgAspIleTyrSerTyrTyrValLysGlyThrSerThrLysThrLys 175
519 CAACGACGACGACAGCGGACGACGACGACGACGACGACGACGACGACG 567
175 rAsnIleValProArgAlaPro.....PheSerAspArgIlePL 188
568 ....CACATCGCGCGCTATGCTGACGCAAGAGTACGCGACGATTC 612

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188 eulysgluasnAlaGlyAla.....AlaSerGlyPhe 198
613 .....AACGGCGCACCCGATACAGCCCGCA 638
199 PheSerArgAlaSpGluAlaGlyLysLeuIleTpeIuSerAsProAs 215
639 GCTGGACAGATCGGGCAATGCCCGCAAGCCTTCAACGGCGCATCGAGATA 688
215 nLysAsnTrpTrpAlaAsnArgMetAspArgIleArgGlyIleValGlnG 232
689 TCGTCAAAAC.....ATCATGGCGCGCGCAGAGAGAAATTCGGCGCA 732
232 LysAlaValAsnProPheLeuMetGlyPheGlnGlyIleGlyAla 248
733 .....GGCGATGCGCGTGCAGGAGTATAGGAGCGCTCAAAATCTGCTG 776
249 IleThrAspSerAlaValAsnProValThrAspThrAlaGlnGlnIln 265
777 CATGCACGGC.....TTGGGTCTGCTTTCACCGCAAAACAGATGG 817
265 rLeuGlnGlyIleAsnHisLeuGlyAsnLeuSerProGluAlaGlnLeu 282
818 CGCGCATCAACGATTTGGCAGATATGGC...CAACTCAAAAGCTATGGC 864
282 LalaAlaThrAlaLeuGlnAspSerAlaPheAlaValLysAspGlyIle 298
865 GCAGCAGCCATCCGATGGATGGAGTCCAAACCCCAATGCCGACAGAG 914
299 AsnSerAla...ArgGlnTrpAlaAspAlaHisProAsnIleThrAla 314
915 CATAGAAAGCGGTACGCAATATCTTTATGGCAGCCATCCCAAAAGG. 963
314 rAlaGlnThrAlaLeuAlaValAlaGlnAlaIleThrValTrpGlyG 331
963 ..... 963
331 LysLysLysValGluLeuAsnProThrLysTrpAspTrpValLysAsnTr 347
964 .....ATTGAGCTGTCCGGGAAATACGGCTTGGCGGCATCAC 1004
348 GlyTyrLysThrProAlaValArg.....Th 356
1005 GGACATCCCTGTCACAGCGGTCGCGATGGCGCGATCGATCGCGCAAG 1054
356 rMetHisThrLeuAspGlyGluMetAlaGlyLysAsnArgPro.... 371
1055 GGAATCCGCGCGTCAGCGACAAATTTTCCGATGCGCA 1092
372 ..LysSerIleThrSerAsnSerLysAlaAspAlaSer 383

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seq_name: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:AA1999

seq_documentation_block:

ID AAY38582 standard; Protein: 482 AA.

AC AAY38582;

DT 08-OCT-1999 (first entry)

DE Neisseria meningitidis strain A antigen encoded by ORF29.

KM Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;

XX treatment; Neisseria infection; meningitis; septicaemia; gonorrhea.

OS Neisseria meningitidis.

PN W09924578-AZ.

PD 20-MAY-1999.

PF 09-OCT-1998; 98WO-IB01665.

PR 01-SEP-1998; 98GB-0019016.

```

PR 06-NOV-1997; 97GB-0023516.
PR 14-NOV-1997; 97GB-0024190.
PR 18-NOV-1997; 97GB-0024386.
PR 27-NOV-1997; 97GB-0025158.
PR 10-DEC-1997; 97GB-0026147.
PR 14-JAN-1998; 98GB-0000759.
XX
PA (CHIR-) CHIRON SPA.
XX
PI Grandi G, Maignani V, Pizza M, Rappuoli R, Scarlato V;
XX WPI; 1999-327407/27.
DR N-PSDB; AAZ12045.
XX
PT Proteins from Neisseria meningitidis and N. gonorrhoeae useful for
XX diagnosis, treatment and prevention of infection
XX
PS Claim 4; Page 145; 524pp; English.
XX
XX Amino acid sequences AAY38499-Y38944 represent Neisseria meningitidis
XX and N. gonorrhoeae antigenic proteins. They are encoded by open
XX reading frames (ORFs) AAZ11972-212358. The antigenic proteins,
XX their fragments, their nucleic acids and antibodies are used for
XX diagnosis, prevention (as vaccines) or treatment of Neisseria
XX infections, such as meningitis, septicaemia and gonorrhea. Both
XX organisms are closely related. Fragments of the nucleic acids
XX are useful as hybridisation probes and antisense reagents.
XX
SQ Sequence 482 AA:

alignment_scores:
  Quality: 403.50      Length: 453
  Ratio: 1.634        Gaps: 21
Percent Similarity: 54.525 Percent Identity: 30.243

alignment_block:
US-09-303-518D-463 x AAY38582 ..

Align seg 1/1 to: AAY38582 from: 1 to: 482

34 TCACATACGCGAGTGTGCTCCGATGATGCACACGCCCTCAGATTGGC 83
   ||||| ..... ||||| ..... ||||| ..... ||||| ..... |||||
15 AlaIleSer**LeuGlnIleProIle...SerHisAlaAsnGlyLeu.. 29
84 AACGATCCCTTTATCCGCGAGTTCTGACCCGTCACATTTGCAACCG 133
   ||||| ..... ||||| ..... ||||| ..... ||||| ..... |||||
30 ....AspAlaArgLeuArgAspAspMetGlnAlaLysHisTyrGluProG 45
134 ACGGAAATACACCTATTTCCGC...AGCAGGGGGAGCTTGCCTGCGC 180
   ||||| ..... ||||| ..... ||||| ..... ||||| ..... |||||
45 LysLysTyrHisLeuPheGlyAsnAlaArgGlySerVal.....Lys 59
181 AACGGCCATATCGGATTCGGGAAACATACAAAGCATGATGGCCACCT 230
   ||||| ..... ||||| ..... ||||| ..... ||||| ..... |||||
60 AsnArgValTyrAlaValGlnThrPheAspAlaThrAlaValGlyProI 76
231 GATG.....ATTCACAGCGCGCGCTTGAGAGAAATATCGGTACA 271
   ||||| ..... ||||| ..... ||||| ..... ||||| ..... |||||
76 eLeuProIleThrHisGluArgThrGlyPheGlnGlyIleIleGlyLys 93
272 TTGTCCGCTTTTCGATACAGCGGACAAATTCATTCGCGCTTCGACAC 321
   ||||| ..... ||||| ..... ||||| ..... ||||| ..... |||||
93 LuthrHisPheSerGlyHisGlyHisGlnValHisSerProPheAspAsn 109
322 CATGCTTCACATTCGATTCGACGAAGCCGGTATGCCGTTGACGAT 371
   ||||| ..... ||||| ..... ||||| ..... ||||| ..... |||||
110 HisAspSerLysSerThrSerAspPheSerGlyLysValAspGlyLys 126
372 CAGCCTTACCGCATTCGATGGAGCGATAGCAACACCATTCGCGCAGC 421
   ||||| ..... ||||| ..... ||||| ..... ||||| ..... |||||
126 eThrValTyrGlnLeuHisArgThrGlySerGluIleHisProGluAsp 143

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422 GGTATGACGGCGCAAGGAGGGCGGCTATCCGGCTCCGAAGAGCGGAG 477
 143 LTTTAspGlyproGlnGlySerAspTrpProProGlnGlyAlaArg 159
 472 GATATATACAGCTACGACATATAAAGCGCTGCGCAAAATATCCGCTCA 521
 160 AspIleTyr****TyrValGlySerLysHisSerThrLysSerAs 176
 522 CCTGACCGCAACACCGCAGCACCGCGCAACGGCTTGCGCAGCGTTTC... 567
 176 nIleValProAlaGlyPro.....PheSerAspArgTrpLeu 189
 568 ...CACAAATGCCGGCGCTATGCTGACGACGAAGATAGGAGCGAGTTC... 612
 189 yGlnAlaSerAlaGlyAla.....AlaSerGlyPhe 199
 613AAAGCGCACCGGATACAGCCCGGAGCT 641
 200 SerArgAlaAspGlnAlaGlyLysLeuLeuLeuTrpGlnSerAspProAsnLys 216
 642 GGACAGATCGGGCAATGCCCGGAGCGCTTCACGCGCATCGACATGCG 694
 216 sAsnTrpTrpAlaAsnArgMetAspAspIleArgGlyLysValGlnGly 233
 692 TCAAAATC....ATCATCGCGCGGACGAGGAATGTGCGGCA... 732
 233 LaValAsnProPheLeuMetGlyPheGlnGlyValGlyLysGlyAlaLe 249
 733 ...GGCGATCGCGCTACAGGATATAGCAGACGATCAACATTCGCTCAT 779
 250 ThrAspSerAlaValSerProValThrAspThrAlaAlaGlnGlnThr 266
 780 GCAGCGC.....TTGGTCTGCTTTCCACGCGCAACAGATGGCGC 820
 266 uGlnGly***AsnHisLeuGly**LeuSerProGlnAlaGlnLeuAla 283
 821 GCATCAGCATTTGGCAATATGGCG...CAATCAAACTATAGCGCA 867
 283 LaAlaThrValAlaLeuIAspSerAlaPheAlaValLysAspGlyLysAsn 299
 868 GGAGCATTCGGGATTTGGGAGTCCAAACCCCAATGGCGCACAAAGCAT 917
 300 SerAla...ArgGlnTrpAlaAspAlaHisProAsnLysLeuAlaThrAl 315
 918 AGAACCGCTCAACAATATCTTATGGACGCGCATCCGCTCCCAAGGATG 967
 315 aGlnThrAlaLeuAlaValAla**AlaAlaThrThrValTrpGly.... 330
 968 GAGCTGTCGGGAAA..... 984
 331GlyLysLysValGlnLeuAsnProThrLysTrpAspTrp 343
 985TAGGCTTGGCGCGCATC..ACGGACATCTCGT 1016
 344 ValLysAsnThrGlyTyr***ThrProAlaValArgThrMetHisThrLe 360
 1017 CAAGCGCTCGCAGATGGCGCGCATGCGATCCGCAAGAGAAATCCGCGC 1066
 360 uAspArgLysMetAlaGlyLysAlaAsnArgProPro....LysSerIleTr 375
 1067 TCAGCGACATTTTGGCATGCG..... 1089
 375 HisSerAsnSerLysLysAspAlaSerThrGlnProSerLeuGlnAlaGln 391
 1090GCATACGCGCAATATC... 1104
 392 LeuIleGlyGlnGlnIle****GlyHisAlaTyrAsnLysHisValIle 408
 1105 ...CCGTCGCCCTTACCATTCGCCGAATATCCGTTCAACATTTGGAGAGC 1150
 408 eaArgGlnGlnGlnLysPheThrAspLeuAsnIleAsnSerProAlaAspPhe 425
 1151 GTTACGGCAAAACAATCATCACTTCCTCAACGTCGCGCGCTCAACAGCGC 12000

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425 1aAGyH1stleclunsnileValSerH1s.....Pro***AsmMet 438
1201 AAAAAATGTC 1209
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439 LysGIuleu 441

seq_name: /SIDSL/gcdata/geneseq/geneseq-emb1/AA199.DAT:AAV38581
seq_documentation_block:
ID AAV38581 standard; Protein: 483 AA.
XX
AC AAV38581;
XX
DT 08-OCT-1999 (first entry)
XX
DE Neisseria meningitidis antigen encoded by ORF29.
XX
KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
treatment; Neisseria infection; meningitis; septicemia; gonorrhea.
XX
OS Neisseria meningitidis.
XX
PN WO9924578-A2.
XX
PD 20-MAY-1999.
XX
PF 09-OCT-1998; 98WO-IB01665.
XX
PR 01-SEP-1998; 98GB-0019016.
PR 06-NOV-1997; 97GB-0023516.
PR 14-NOV-1997; 97GB-0024190.
PR 18-NOV-1997; 97GB-0024386.
PR 27-NOV-1997; 97GB-0025158.
PR 10-DEC-1997; 97GB-0026147.
PR 14-JAN-1998; 98GB-0000759.
XX
PA (CHIR-) CHIRON SPA.
XX
PI Grandi G, Maignani V, Pizza M, Rappuoli R, Scarlato V;
XX
DR WPI; 1999-327407/27.
XX
DR N-PSDB; AA212044.
XX
PT Proteins from Neisseria meningitidis and N. gonorrhoeae useful for
diagnosis, treatment and prevention of infection
XX
PS
XX
PS Claim 4; Page 144; 524pp; English.
XX
CC Amino acid sequences AAV38499-Y38944 represent Neisseria meningitidis
CC and N. gonorrhoeae antigenic proteins. They are encoded by open
CC reading frames (ORFs) AA21972-212358. The antigenic proteins
CC their fragments, their nucleic acids and antibodies are used for
CC diagnosis, prevention (as vaccines) or treatment of Neisseria
CC infections, such as meningitis, septicemia and gonorrhea. Both
CC organisms are closely related. Fragments of the nucleic acids
CC are useful as hybridisation probes and antisense reagents.
XX
XX
SQ Sequence 483 AA;

alignment_scores:
Quality: 390.00 Length: 433
Ratio: 1.618 Gaps: 25
Percent Similarity: 55.658 Percent Identity: 30.716

alignment_block:
US-09-303-518D-463 x AAV38581 ..

Align seg 1/1 to: AAV38581 from: 1 to: 483

31 CTGTCACACTGCGAGTGTGCCCTGCGCATGATGCACAGCGCTCAGATT 80
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16 IleSerLeuEngInleProIle.....SerHisAlaasnGlyLe 29
81 GGAAAGACGCTTATCCGAGGTTCTCGACCGTACAGCATTTGAGAC 130
29 u.....AspAlaIArgLeuArGAspSpmecGlnAlaLysHisTylGlu 44
131 CCAGAGGGAATATACACCTATTCGGC...AGCAGGGGGAGCTTGGCNA 177
44 roglYglYlYsTylrHisLeuPhelGlyAsnAlaArgLysSerValYlYs 60
178 CGACAGCGGCATATCCGATTGGGAACATACAAAGCCATCAG..... 219
61 Arg.....ValTyrAlaValGlnThrPheAspAlaThrAl 72
220 .....TTGGGCCACCTGATGATTCACACAGCGGCGG 250
72 aValSerProValLeuProIleThrHis.....GluThrThylYp 86
251 TTGAAGAAATATCCGCTACATTGTCGCTTTCCGATCAGGGCAGCA 300
86 hegluGlyValIleGlyTyrGluThrHisPheSerGlyHisGlyHisGlu 102
301 TTCGATTCGGCTTCGACACACATGCTCAGATTCGATTCGACAGAC 350
103 ValHisSerProPheAspHisHisAspSerLysSerThrSerAspPhe 119
351 CGGTAGTCCGCTTGAGGATTCAGCCTTACCGCATTCGATTCGAGAG 400
119 rGlyGlyValAspGlyGlyPheThrValYlYrGlnLeuHisArgThGlyS 136
401 ACGAACACATCCCGCGCGGCTATGACGGCCACAGGGCGGCGCTAT 450
136 ergluIleHisProGluAspGlyTyrAspGlyProGlnGlySerAspTyr 152
451 CCGGCTCCCAAGCGCGAGGATATATACGCTACGACATAAAGCGCT 500
153 ProProGlyGlyAlaArgAspIleTyrSerTyrValYlYsGlyTh 169
501 TGCCCAAAATATCGCCTCAACCTGACCGCACACCGAGACCGGCAAC 550
169 rSerThrLysThrLysThrAsnIleValProGlnAlaPro..... 182
551 GCGTTCGCGACCGTTTC.....CACAAATCGCGCGCTATGTCAGCAA 594
183 ..PheSerAspArgTyrPleuLysGluAsnAlaGlyAla..... 194
595 GGAGTAGCGCAGGATTC.....AAAGCGC 620
195 .....AlaSerGlyPhePheSerArgAlaAspGluAlaGlyLysLeuI 209
621 CACCCGATACAGCCGCGAGCTGGACAGATCGGCAATGGCGGAGGCG 670
209 eTTPGluSerAspProAsnLysAsnTTPTPAlaAsnAlaGlyMetAspY 226
671 TCAACGCGACTGCAGATATGTCAAAAC.....ATCATCGCGCGGCA 714
226 alArgGlyIleValGlnGlyAlaValAsnProPheLeuMetGlyPheGln 242
715 GGAGAAATTTGCGGCGCA.....GGCGATCGCGCTGACAGGATTAAGCA 758
243 GlyValGlyIleGlyAlaIleThrAspSerAlaValSerProValThrAs 259
759 AGGCTCAAAACATTCGTGTCATGCACGCG.....TTGGGCTGCTGTT 799
259 pThrAlaIleGlnGlnThrLeuGlnIleAsnAspLeuGlyLysLeuS 276
800 CCAACGCAAAACAGATGCGCGCATCAACGATTTGGCAGATATGCGC... 846
276 eTTPGluAlaGlnIleuAlaAlaAlaSerLeuEngInAspSerAlaPhe 292
847 CAACCTCAAGACTATGCGCGCAGCAGCCATCCGCGATTGGCAGCTCAAA 896
293 AlavAlYlYsAspGlyIleAsnSerAla...LysGlnTTPAlaAspAlaH 308

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897 CCCCAAT.....GCCGACAAAGCATAGACGG 925
308 sProAsnIleThrAlaThrAlaGlnThrAlaLeuSerAlaAlaGluAla 324
926 TCAGCAATATCTTATGCGACGATCCCATCAAAAGGATTGGAGCTGTC 975
325 AlaGly...ThrValTyrArg.....GlyLysLysValGluLeuAs 337
976 CGGGCAAAATACGCTTGCGCG.....GCAT 1001
337 nProThrLysTyrAspTyrValLysAsnThrGlyTyrLysLysProAla 354
1002 CAGCGCACATCTCTGTCAGCGTGCAGATGGCGCGCATTCGATTCGCGA 1051
354 IaArgHisMetGlnThrLeuAspGlyGluMetAla..... 365
1052 AAGGAAATCCGCGCGTCAGCACAATTTGGCGATGCGCATACGCCAA 1101
366 GlyGlyAsnLys.....ProIleLysSerLeuProAs 376
1102 TACG.....CGTCCCTTACCATTCGCAATATCCGTTCAA 1139
376 nSerAlaAlaGluLysArgLysGlnAsnPhelGluLysPheAsn...SerA 392
1140 CTGAGCAGCGCT.....ACGGCAAGAAACATCACCTGCT 1177
392 sTTPSerSerAlaSerPheAspSerValHisLysThrLeuThrPro 407
seq_name: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:AAV74708
seq_documentation_block:
ID AAV74708 standard; Protein; 483 AA.
XX
AC AAV74708;
XX
DT 21-MAR-2000 (first entry)
XX
DE Neisseria meningitidis ORF 238 protein sequence SEQ ID NO:890.
XX
KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KW antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;
KW antibacterial; gene therapy.
XX
OS Neisseria meningitidis.
XX
PN W09957280-A2.
XX
PD 11-NOV-1999.
XX
PF 30-APR-1999; 99MO-US09346.
XX
PR 01-MAY-1998; 98US-0083758.
PR 31-JUL-1998; 98US-0094869.
PR 02-SEP-1998; 98US-0098994.
PR 02-SEP-1998; 98US-0098962.
PR 09-OCT-1998; 98US-0103749.
PR 09-OCT-1998; 98US-0103794.
PR 09-OCT-1998; 98US-0103796.
PR 25-FEB-1999; 99US-0121528.
XX
PA (CHIR ) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
XX
PI Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;
PI Petersen J, Pizsa M, Rappuoli R, Ratti G, Scalato E, Scarselli M;
PI Tettelin H, Venter JC;
XX
DR WPI: 2000-062150/05.
DR N-PSDB: AA253470.
XX
PT Novel Neisserial polypeptides predicted to be useful antigens for
vaccines and diagnostics

```

XX PS Claim 2: Page 544-545; 1453bp; English.

CC AA253015 to AA254536, AA254577 to AA254615, and AA274253 to AA275941
 CC represent novel *Neisseria meningitidis* and *N. gonorrhoeae* polynucleotides
 CC and polypeptides. AA254537 to AA254576 and AA254616 to AA254673 represent
 CC PCR primers used in the exemplification of the present invention. The
 CC polypeptides, the polynucleotides, antibodies and compositions of
 CC the invention can be used as vaccines, as diagnostic reagents, and as
 CC immunogenic compositions. The polypeptides can be used in the
 CC manufacture of medicaments for treating or preventing infection due to
 CC *Neisseria* bacteria (e.g. meningitis and septicemia), to detect the
 CC presence of *Neisseria* bacteria, or to raise antibodies. They may also
 CC be used to screen for agonists or antagonists, which may themselves
 CC have use as antibacterial agents. The polynucleotides of the invention
 CC may also be used in gene therapy protocols.

XX SQ Sequence 483 AA:

alignment_scores: Length: 433
 Quality: 390.00 Gaps: 25
 Ratio: 1.618 Percent Identity: 30.716
 Percent Similarity: 55.658

alignment_block:
 US-09-303-518D-463 x AA274708 ..

Align seg 1/1 to: AA274708 from: 1 to: 483

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16 lIeSerLeuLeuGlnIleProIle.....SerHisAlaAsnGlyLe 29
   |||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
81 GGCAACGATCCCTTTATCCGCGAGTTCTCGACCGTCGACATTTCGAAC 130
   |||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
29 u.....AspAlaArgLeuArgAspAspMetGlnAlaLysHisTyrGluP 44
   |||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
131 CCGAGCGGAATACCACTATTCGGC...ACGAGGGGGAGCTTGGCCNAG 177
   |||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
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   |||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
178 CGCAAGCGCATTCGATGGGAACATCAAGCCATCAG.....219
   |||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
61 Arg.....ValTyrAlaValGlnThrPheAspAlaThrAl 72
   |||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
220 .....TTGGGCCACTGATGATTTCACAGCGCGCGC 250
   |||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
72 aValSerProValLeuProIleThrHis.....GluArgThrGlyP 86
   |||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
251 TTGAAGGAATATCGGCTACATTTGCCGTTTCCGATCAGGGCACA 300
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86 heGlyGlyValIleGlyTyrGlnThrHisPheSerGlyHisGlyHisGlu 102
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301 TTCCATTGCGCCTTGCACACACGCTCATATTCCGATTCTGACGAAGC 350
   |||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
103 ValHisSerProPheAspHisHisAspSerLysSerThrSerAspPhe 119
   |||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
351 CGGTAGTCCCGTTGACGATTCACGCTTACCGCATTCATGGGACGAT 400
   |||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
119 rGlyGlyValAspGlyGlyPheThrValTyrGlnLeuHisArgThrGly 136
   |||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
401 ACGAACACCATCCCGCGACGCGTATGACGGGCGACAGGGGCGGCTAT 450
   |||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
136 erGlnIleHisProGlnAspGlyTyrAspGlyProGlnGlySerAspLys 152
   |||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
451 CCCGCTCCCAAGCGCGAGGATATATACAGCTACGACATAAAGCGCT 500
   |||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
153 ProProGlyGlyAlaArgAspIleTyrSerTyrTyrValLysGlyThr 169
   |||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
501 TGCCCAAAATATCCGCTCAACCTGACGCAACCGGACCGACCGACAA 550
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169 rSerThrLysThrLysThrAsnIleValProGlnAlaPro.....182

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551 GGCTTGCCGACCGTTTC.....CACAAATGCCGCGCTATGCTGACGCA 594
   |||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
183 ..PheSerAspArgTyrPheLysGlnAsnAlaGlyAla.....194
   |||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
595 GGAGTAGCGCGACGATTC.....AAACGCC 620
   |||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
195 .....AlaSerGlyPhePheSerArgAlaAspGlnAlaGlyLysLeuI 209
   |||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
621 CACCGCATACACCCCGACCTGACAGATCGGGCAATGCGCGCGAGCT 670
   |||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
209 eTTPGtSerAspProAsnLysAsnTTPTPAlaAsnArgMetAspAspV 226
   |||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
671 TCACGCGACCTGACGATATGCTCAAAAC.....ATCATCGCGCGGCA 714
   |||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
226 AlArgGlyLysLeuAlaGlnGlyAlaValAsnProPheLeuMetGlyPheGln 242
   |||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
715 GGAGAAATTTGTCGCGCA.....GCGATVCGCTGACAGGTATAGCGA 758
   |||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
243 GlyValGlyIleGlyAlaIleThrAspSerAlaValSerProValThrAs 259
   |||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
759 AGGCTCAACATTTGCTGTCATGACGCGC.....TTGGTCTGCTTT 799
   |||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
259 pThrAlaAlaGlnGlnThrLeuGlnGlyLysAsnAspLeuGlyLysLeuS 276
   |||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
800 CCACCGAAACAAAGATGGCGCGCATCAACGATTTGGCAGATATGCG... 846
   |||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
276 erProGlnAlaGlnLeuAlaAlaAlaSerLeuLeuGlnAspSerAlaPhe 292
   |||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
847 CAACCTCAAGACTATGCGCGACGACCATCCGATGGCGAGTCCCAAA 896
   |||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
293 AlaValLysAspGlyLysLeuSerAla...LysGlnTTPAlaAspAlaI 308
   |||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
897 CCGCCAT.....GCCGACAGCGCATAGAACGCG 925
   |||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
308 sProAsnIleThrAlaThrAlaGlnThrAlaLeuSerAlaAlaGlnAla 324
   |||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
926 TCAGCAATATCTTTATGACAGCCATCCCATCAAGAGGATGGAGCTGC 975
   |||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
325 AlaGly...ThrValTyrPheGly...GlyLysLysValGlnLeuAs 337
   |||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
976 CGGGGAAATATCGCTTGGCGC.....GCAT 1001
   |||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
337 nProThrLysTTPAspTTPValLysAsnThrGlyTyrLysLysProAla 354
   |||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
1002 CAGGCGCATCTGTCGACAGCGTCCGAGATGGCGCGATCGATGCCGA 1051
   |||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
354 lAspGlnHisMetGlnThrLeuAspGlyGlnMetAla.....365
   |||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
1052 AAGGGAATCCGCGCTGACGCAATTTTGGCGATCGGCATACGCCA 1101
   |||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
366 GlyLysLysLys.....ProIleLysSerLeuProAs 376
   |||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
1102 TACC.....CGTCCCTTACCATTCGCCGAATATCCGTTCCGTTCA 1139
   |||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
376 nSerAlaAlaGlnLysArgLysLysLysLysLysPheAsn...SerA 392
   |||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
1140 CTGAGACGACGCTT.....ACGGCAAGAAGAAACATCACCTCT 1177
   |||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
392 snTTPSerSerAlaSerPheAspSerValHisLysThrLeuThrPro 407
   |||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
seq_name: /SIDSI/gcgdata/geneseq/geneseqp_emb1/AA2000.DAT.AAB37859
seq_documentation_block:
ID AAB37859 standard; Peptide; 73 AA.
XX
AC AAB37859;
XX
DT 26-FEB-2001 (first entry)
XX
DE Neisseria conserved peptide #42.
XX
KW Neisseria meningitidis; Neisseria gonorrhoeae; antibacterial;

```

KW gene therapy; conserved sequence.
XX
OS Neisseria sp.
XX
PN WO200066741-A2.
XX
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000WO-1B00642.
XX
PR 30-APR-1999; 99GB-0010168.
PR 09-MAR-2000; 2000GB-0005728.
XX
PA (CHIR-) CHIRON SPA.
XX
PI Rappuoli R;
XX
DR WPI; 2000-687543/67.
XX
PT Novel Neisserial protein fragments and their corresponding nucleic
PT acids, useful in the manufacture of medicines for the prevention of
PT Neisserial infection, and in the manufacture of diagnostic reagents -
XX
PS Claim 15; Page 58; 157pp; English.
XX
CC The present peptide is a conserved region of a Neisserial protein.
CC Neisserial proteins containing this sequence, and the nucleic acids
CC that encode such proteins, are useful in the manufacture of medicines
CC for the prevention of Neisserial infection, and in the manufacture of
CC multi-specific diagnostic reagents.
XX
SQ Sequence 73 AA;

alignment_scores:
Quality: 372.00 Length: 73
Ratio: 5.239 Gaps: 0
Percent Similarity: 97.260 Percent Identity: 94.521

alignment_block:
US-09-303-518D-463 x AAB37859 ..

Align seg 1/1 to: AAB37859 from: 1 to: 73

1075 AATTTGGCGATGGCGCATACGCCAATATCCCGTCCCTTACCATTCGCG 1124
|||||
1 AsnPhelAlaSPAlaAlaTyrAlaLysTyrProSerProTyrHisSerAr 17
1125 AATATCCCTTCAAACTTGACGACGCGTTAGCGCAAGAAACATCACCCT 1174
|||||
17 gAnuIleArSerAsnLeuGluGlnArGTrGlyLysGluAsnIleTrHis 34
1175 CCTCAACCGTGGCGCGTCAACGGCAAAATGTCAAACTGGCAGACCA 1224
|||||
34 eSerThrValProProSerAsnGlyLysAsnValLysLeuAlaAsnLys 50
1225 CGCCACCCCAAGACAGCGGTACCGTTTGAAGGTAAGGTTTCCGAATTT 1274
|||||
51 ArgHisProLysThrLysValProPheAspGlyLysGlyPheProAsnPh 67
1275 TGAGAAAGCAGCGTGAATAT 1293
|||||
67 eGluLysAspValLysTyr 73

seq_name: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT: AAB37855
seq_documentation_block:
ID AAB37855 standard; Peptide; 63 AA.
XX
AC AAB37855;
XX
DT 26-FEB-2001 (first entry)
XX

DE Neisserial conserved peptide #38.
XX
KW Neisseria meningitidis; Neisseria gonorrhoeae; antibacterial;
KW gene therapy; conserved sequence.
XX
OS Neisseria sp.
XX
PN WO200066741-A2.
XX
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000WO-1B00642.
XX
PR 30-APR-1999; 99GB-0010168.
PR 09-MAR-2000; 2000GB-0005728.
XX
PA (CHIR-) CHIRON SPA.
XX
PI Rappuoli R;
XX
DR WPI; 2000-687543/67.
XX
PT Novel Neisserial protein fragments and their corresponding nucleic
PT acids, useful in the manufacture of medicines for the prevention of
PT Neisserial infection, and in the manufacture of diagnostic reagents -
XX
PS Claim 15; Page 58; 157pp; English.
XX
CC The present peptide is a conserved region of a Neisserial protein.
CC Neisserial proteins containing this sequence, and the nucleic acids
CC that encode such proteins, are useful in the manufacture of medicines
CC for the prevention of Neisserial infection, and in the manufacture of
CC multi-specific diagnostic reagents.
XX
SQ Sequence 63 AA;

alignment_scores:
Quality: 313.00 Length: 63
Ratio: 5.131 Gaps: 0
Percent Similarity: 96.825 Percent Identity: 95.238

alignment_block:
US-09-303-518D-463 x AAB37855 ..

Align seg 1/1 to: AAB37855 from: 1 to: 63

13 CGCAAAATATCCCTTATTCGTCCATACGTGCGAGTGTGCTGCCGATGCA 62
|||||
1 ArgLysIleSerLeuIleLeuSerIleLeuAlaValCysLeuProMetH 17
63 TGCACAGCGCTCAGATTGGCAACGATCCCTTATTCGCGAGTTCTCG 112
|||||
17 sAlaHisAlaSerAspLeuAlaAsnAspSerPheIleArgGlnValLeuA 34
113 ACGTTCAGATTTCGAACCCGACGGGAATATACCATTCGCGACAGG 162
|||||
34 sParGlnHisPheGluProAspGlyLysTyrHisLeuPheGlySerAr 50
163 GGGAGCGTTGCCNAGCGCAAGCGCATATCGATTGGGA 201
|||||
51 GlyGluLeuAlaGluArGSerGlyHisIleGlyLeuGly 63

seq_name: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT: AAY38580
seq_documentation_block:
ID AAY38580 standard; Protein; 125 AA.
XX
AC AAY38580;
XX
DT 08-OCT-1999 (first entry)
XX
DE Neisseria meningitidis antigen encoded by a partial ORF29.

```

XX  Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KM  treatment; Neisseria infection; meningitis; septicaemia; gonorrhea.
XX
XX  Neisseria meningitidis.
OS
XX  W09924578-A2.
XX
XX  20-MAY-1999.
XX
XX  09-OCT-1998; 98WO-IB0165.
XX
XX  01-SEP-1998; 98GB-0019016.
XX  06-NOV-1997; 97GB-0023516.
XX  14-NOV-1997; 97GB-0024190.
XX  18-NOV-1997; 97GB-0024386.
XX  27-NOV-1997; 97GB-0025158.
XX  10-DEC-1997; 97GB-0026147.
XX  14-JAN-1998; 98GB-0000759.
XX
XX  (CHIR-) CHIRON SPA.
XX
XX  Grandi G, Maignani V, Pizzi M, Rappuoli R, Scarlato V;
XX  WPI: 1999-327407/27.
XX  N-PSDB; AA12043.
XX
XX  Proteins from Neisseria meningitidis and N. gonorrhoeae useful for
XX  diagnosis, treatment and prevention of infection
XX
XX  Claim 4; Page 143; 524pp; English.
XX
XX  Amino acid sequences AA138499-138944 represent Neisseria meningitidis
XX  and N. gonorrhoeae antigenic proteins. They are encoded by open
XX  reading frames (ORFs) AA11972-212358. The antigenic proteins,
XX  their fragments, their nucleic acids and antibodies are used for
XX  diagnosis, prevention (as vaccines) or treatment of Neisseria
XX  infections, such as meningitis, septicaemia and gonorrhea. Both
XX  organisms are closely related. Fragments of the nucleic acids
XX  are useful as hybridisation probes and antisense reagents.
XX
XX  Sequence 125 AA:

```

```

alignment_scores:
  Quality: 264.00      Length: 115
  Ratio: 3.259        Gaps: 1
  Percent Similarity: 70.435      Percent Identity: 45.217

```

alignment_block:

US-09-303-518D-463 x AAY38580 ..

Align seg 1/1 to: AAY38580 from: 1 to: 125

```

238 CACAGGCGGCGCTTGAAGAAATATCGGCTACATTTGTCGCTTTTCGA 287
      ::::::::::: ||||| ||||| :::::::::::
10 GLUATGTHGlyPheGLuGLyValIleGLyTyrGLuThrHisPheSerGI 26
288 TCAGGCGGACAAATTCATTCGCTTCGACACCAATGCCATTCGCG 337
      ||||| :::: ||||| ||||| :::: |||||
26 YHISGLYHISGLYValHisSerProPheAspHisSerPseSerI 43
338 ATTCGACGAGCGCGGTAGTCCGCTTACGATTCAGCTTACCGATC 387
      ||||| :::: ||||| :::: ||||| :::: |||||
43 hrSerAspSerIcIyValAspGLyGLyPheThrValTyrGLuLeu 59
388 CATTGGAGGATACGACACCATCCGCGCGGCTATGACGGGCCACA 437
      ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
60 HisArgThrTrpSerGLuIleHisProGLuAspGLyTrpAspGLyProGI 76
438 GGGCGGCGGCTATCCGCTCCCAAGGCGGCGGATATATACGCTACG 487
      ||::: ||||| ||| ||||| ||||| ||||| |||||
76 nAlaIaA**TyrProProProGLyGLyAlaArgAspIleTyrSerTyr 93

```

```

488 ACATTAAGCGGTGCCCAAAATATCGCCCTCACTACCGGACACCGC 537
      ::||| ::::: ::::: ::::: ::::: :::::
93 yValIyGLyThrSerThrIystrIystrIleValProGLuAla 109
538 AGCACCGGACAGCGCTTGGCCGCTTCCCAATGCGGCGGCT 582
      ::::: ||| ::::: |||||
110 ProPheSerAspArgTrpLeuGLu.....GLuSmaIaGLyAla 122

```

seq_name: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT: AAB37858

seq_documentation_block:

ID AAB37858 standard; Peptide: 41 AA.

XX AAB37858;

XX 26-FEB-2001 (first entry)

XX Neisserial conserved peptide #41.

XX Neisseria meningitidis; Neisseria gonorrhoeae; antibacterial;

XX gene therapy; conserved sequence.

XX Neisseria sp.

XX Key Location/Qualifiers

XX Misc-difference 23 /label= Val, Ile

XX W0200066741-A2.

XX 09-NOV-2000.

XX 28-APR-2000; 2000WO-IB00642.

XX 30-APR-1999; 99GB-0010168.

XX 09-MAR-2000; 2000GB-0005728.

XX (CHIR-) CHIRON SPA.

XX Rappuoli R;

XX WPI: 2000-687543/67.

XX Novel Neisserial protein fragments and their corresponding nucleic

XX acids, useful in the manufacture of medicines for the prevention of

XX Neisserial infection, and in the manufacture of diagnostic reagents -

XX Claim 15; Page 58; 157pp; English.

XX The present peptide is a conserved region of a Neisserial protein.

XX Neisserial proteins containing this sequence, and the nucleic acids

XX that encode such proteins, are useful in the manufacture of medicines

XX for the prevention of Neisserial infection, and in the manufacture of

XX multi-specific diagnostic reagents.

XX Sequence 41 AA:

alignment_scores: Quality: 196.00 Length: 41

Percent Similarity: 95.122 Percent Identity: 95.122

alignment_block: US-09-303-518D-463 x AAB37858 ..

Align seg 1/1 to: AAB37858 from: 1 to: 41

```

949 ATCCCATCAAGAGATTGAGCTTCCGCGGAAATATACGCTTGGCGG 998
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 IleProIleIySGLyIleGLyAlaValArgGLyLysTyrGLyLeuGLyGI 17

```

```

999 CATCAGCGCATCTGTCAAGCGGTGAGATGGCGGATCGCATTCG 1048
      |||||
17  YLITHTALAHISPro**LysArgSerGlnMetGlyIuLleAlaLeuP 34
      |||||
1049 CGAAGAGGAATCCGCCGTCAGC 1071
      |||||
34  rOLysSLySerserAlaValSer 41

seq_name: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA199.DAT:AA104841

seq_documentation_block:
ID  AA104841 standard; Protein: 506 AA.
XX
XX  AA104841;
AC
XX  06-JUL-1999 (first entry)
DT
XX  Mycobacterium species protein sequence 150#3.
DE
XX  Secreted protein; Mycobacterium; primer; PCR; amplification; probe;
KW  hybridisation; detection; vaccine; immunisation; infection.
XX
OS  Mycobacterium sp.
XX
XX  W09909186-A2.
PD
XX  25-FEB-1999.
PE
XX  14-AUG-1998; 98WO-FR01813.
XX
XX  11-SEP-1997; 97FR-0011325.
PR  14-AUG-1997; 97FR-0010404.
XX
XX  (INSP ) INST PASTEUR.
XX
XX  Glacquel B, Lim EM, Pelicic V, Portnoi D, Goguet de la Salmoniere Y,
PI  Gutuano A;
XX
XX  WPI: 1999-181045/15.
DR  N-PSDB; AAX34093.
XX
XX  Mycobacterial DNA vectors containing reporter constructs : for
PT  identifying coding or promoter sequences involved in
PT  infection associated protein expression
XX
XX  Claim 32: Fig 15Q; 309pp; French.
XX
XX  Sequences AAY04742-Y05000 and AAY07201-Y07204 represent secreted
CC  proteins from various Mycobacterium species microorganisms. The
CC  encoding nucleotide sequences can be used as primers and probes for
CC  methods for detecting and identifying mycobacteria, especially belonging
CC  to the M. tuberculosis complex. The encoded proteins can be used in
CC  vaccines for immunisation against a bacterial or viral infection.
XX
XX
SQ  Sequence 506 AA:

alignment_scores:
      Quality: 188.00      Length: 468
      Ratio: 0.935        Gaps: 27
Percent Similarity: 42.949 Percent Identity: 27.137

alignment_block:
US-09-303-518D-463 x AAY04841 ..
Align seg 1/1 to: AAY04841 from: 1 to: 506

```

```

117 gCySgLYValGlnProProSerGlyHisArgLeuProSerHisArgLeuG 134
129 .....ACCCGAGCGGAATACCACTTATCGGACAGAGGGGAGCT 170
      |||
134 LYArgAlaLeuArgGlyProValGlyHisIleArgCysArgThrGlyArg 150
171 TGCCNAGCGCAAGGCCATATCGG.....ATTGGAA 202
      :
151 PheSerIleArgArgProArgArgGlyValValValThrGlyAspGlyArg 167
203 ACATACAAAGCCATCA.....GTGGGCCACTGATGATTCAA 240
      :
167 gLeuAlaArgProAlaGlySerAlaGlyAlaGlyAlaArgThr 184
241 CAGCGCGCGCTTGAAGGAATATCGCTACATTGCTCCGCTTTCCGATCA 290
      :
184 roAlaGlyArg.....ArgPheTrpProThr 192
291 CGGCGCAAAATTCATTCGCGCTTCGACAAACATGCTCATTCGATG 340
      |||||
193 ArgAlaAla..... 195
341 CTGACGAAGCCGATGTCCTCGTTCAGCATTCAGCTTACCGCATCA. 389
      |||
196 ....ArgArgCysTrpAlaArgAlaArgArgGlnProAlaArgLysPro 211
390 .....TTGGACGGATACGAACACCATCCGCGCAGCGCTA..... 425
211 rPTTrpArgArgHisArgArgArgThrArg**GlyArgLeuAspSer 227
426 .....TGACGGCCACAGAGCGCGGCTATCCCGCCCA 460
228 GLYArgCysIleProGlyArgAlaCysGlyPheGlyArgThrArgSerAl 244
461 AAGCGCGAGGATATATACAGCTACGA.....CATAA..... 494
244 aArgTrpGlySerArgSerAlaIleArgProAlaHisArgSerPro 261
495 .....AGCGTTGCCCAAAATATCCGCTCAACCT 524
261 erGlyGlyArgArgSerAlaArgArgSerProSerGlyProArgPro 277
525 GACCGACACCGCAGCAGCAGCAGCGGCTTGCCGACG..... 563
278 ProArgArgPro.....ValAlaAlaArgProValArgSerVa 290
564 .....TTTCCCAATGCGCGGCTATGCTGACGCGAAGAGCTAGGCGACGA 609
290 IgIyIleSerGlyCysArgSerAlaArgGlnLys**GlyProProThrL 307
610 TTCAACGCGCGCCAGCATACAGCCCGCAGCTGGACAG.....ATCGGG 653
307 euTrpAlaArgArgPro.....ProArgValGlyArgProLeuSerGly 321
654 CAATGCCGCCGA.....AGCTTCAAGCGCAGCTGCAG 685
322 ArgSerArgArgArgAlaGlyLeuProAlaSerSerArgValCysArg 338
686 ATATCGTCAAAAACATCATCGCGCGCGCAGGAGAAATTTGCGCGCAGCG 735
338 gGlnArgCysArgGlySerValArgGly.....ArgArgArgA 351
736 GATCGCGTGCA...GGGTATAGCGAAGAGCTCAACATTTGCTCATGCA 782
351 rGcysAlaAlaArgGlyCysArgArgArg.....Gly 361
783 CGGCTTGCGTCTGCTTCCACGCAAAACAAGATGCGCGCATCAAGATT 832
362 Arg...TrpIlyCysAlaArgPro.....AlaAlaThrVal 372
833 TGCGAGATATGCGCGCACCTCAAGACTATGCCGCGAG..... 868
373 CysAlaPheTrpIlySerAlaArgThrProProGlyGlyArgAlaProTr 389

```



```
869 ....CAGCCATCCGCGATTTGGCAGTCCCAAAACCCCAATGCGGCACAGG 914
      ||| ||||| ||||| |||||
389 pcysalaprovalaiaile.glyserpro.....AlaArg 400
      ||| ||||| ||||| |||||
915 CATAGAACCCGTCACCAATATCTTTATGGACGCCATCCCATCAAGGGA 964
      ||| ||||| ||||| |||||
401 gIyArGArGArGArGArGTrp.....ProArgProGlyGI 412
      ||| ||||| ||||| |||||
965 TTGAGAGTGT.....CCGGGAAATATACGCTTGGCGGCATCAG 1005
      ||||| ||||| ||||| |||||
412 yCyserGySvAlaAlaArgProGlyArGArGArGArGArGAlas 429
      ||| ||||| ||||| |||||
1006 GCACATCTCTCAACCGGTCGCAGATGGCGCGATCCGATCCGCAAAATACC 1055
      ||| ||||| ||||| |||||
429 eArGArGcYsArGcYlAspGlyAsnThrAlaProTPrCyAlAlaAlaThr 445
      ||| ||||| ||||| |||||
1056 GAAATCCGCGCCGACGCAATTTGGCGATGGCGCATCCGCAAAATACC 1105
      ||||| ||||| ||||| |||||
446 ArGleuAlaGTrpArGArG.....Pr 452
      ||||| ||||| ||||| |||||
1106 CGTCCCTTACCATTTCCGAAATATCCGTTCAACTTGGACGACGTTA 1154
      ||||| ||||| ||||| |||||
452 oValProArgProProAlaAlaGlySerGlyArGAlaGlyAlaSerLeuG 469
      ||||| ||||| ||||| |||||
1155 .....CGGCAAGAAATACATCACTCTCAACCGTCCCGCGTC 1193
      ||||| ||||| ||||| |||||
469 lnaArgGlyTrpArGArGArGAlaAlaProGlnSerValArGValArGAla 485
      ||||| ||||| ||||| |||||
1194 AAACGGCAAAATGTCAAACTGCGACACCAACCGCACCCGCAAGACGCG 1243
      ||||| ||||| ||||| |||||
486 AlArGlyArgnGlyGluAlaGlyThrProThrAsnProSerSerArG 502
      ||||| ||||| ||||| |||||
1244 T 1244
      ||||| ||||| ||||| |||||
502 g 502
```

seq_name: /STDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:ABG08343

seq_documentation_block:

ID ABG08343 standard; Protein; 398 AA.

XX ABC08343;

DT 13-FEB-2002 (first entry)

DE Novel human diagnostic protein #8334.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US08631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

PA (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR WPI; 2001-639362/73.

DR N-PSDB; AAS72530.

PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity

```
XX Claim 20; SEQ ID NO 38702; 103pp; English.
PS The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or as
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations in
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 398 AA:
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alignment_scores: Quality: 171.50 Length: 443
Ratio: 0.884 Gaps: 26
Percent Similarity: 43.792 Percent Identity: 26.862

alignment_block:

US-09-303-518D-463 x ABG08343 ..

Align seg 1/1 to: ABG08343 from: 1 to: 398

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15 CAAATATCCCTTATTCCTCATCT.....GGCATGTGCTTGC 55
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27 ArgAsnLeuSerArgSerLysHisThrProHisSerThrProAl 43
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56 CGATGCATCCACACCGCTTCGATTTGGCAACGATCCCTTATCCGGGAG 105
   ||||| ||||| ||||| |||||
43 AhHisLeuSerLysProProArgSerSerGluValIlyHisSerG 60
   ||||| ||||| ||||| |||||
106 GTTTCGACCGTCACATTTGCAACCGGCAAGAAATACCACTATTTCGG 155
   ||||| ||||| ||||| |||||
60 lnaValLeuProGlyThrProArg.ProThrSerGlnLeuHisLeuGlu 76
   ||||| ||||| ||||| |||||
156 CAGCAGGGGGGAGCTTGGCCMAGCGGCAATATTCGATTGGGAACA 205
   ||||| ||||| ||||| |||||
76 uValLeuProValPneAlaArgLeuProGlyHisArgGlyIleGluArg 93
   ||||| ||||| ||||| |||||
206 TACAAGCCATCAGTTGGGCCACCTGATGATTCAAACAGCGCGCTTGA 255
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93 lnaGlnSerSerPro..... 97
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256 GGAATATTCGCTACATTTGCTTCGATCAGCGGCAAAATTCGA 305
   ||||| ||||| ||||| |||||
98 .....TyrSerArgArgGlyHis..... 103
   ||||| ||||| ||||| |||||
306 TTGCGCCTTGACAACCATGCTTCACATTCGATTTCGACGACCGGTA 355
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104 .....HisArgGlyIlyThrGluGluAsp***ValAsnS 115
   ||||| ||||| ||||| |||||
356 GTCCCGTTGACGAGATTCAGCTTACCGCATTCATGGACGATACGAA 405
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115 er*****AspGlyValGluProIlyr..... 123
   ||||| ||||| ||||| |||||
406 CACATCCCGCGGCGCTATGACGGGCAAG...GGCGGCGGCTATCC 452
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124 ...GlyLysValAlaAlaAlaGlyProGlnArgGlyArgGlyIlyrGc 139
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453 CGCTCCCAA.....AGCGCGAGGATATATACAGCTACGACATATAA 495
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139 scyprpttrpargarglinarghisgly.....ArgHisarGa 152
496 GCGCTTGGCCAAATATCCGCT.....CAACCTGAC 527
    |||||
152 rgarg.....ProtrillealeuGlnArgGlnProAla 164
528 CGACACCG.....CAGCACCGGACACAGCG 553
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165 ArgthrProSerAlaArgProIleAlaLeuGlnArgGlnGlnAl 181
554 TTGCCGACCGTTTCCACAATCCGCGCGTATCTGACGCAAGAGTAGGC 603
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181 argthrProSerPro.....ArgProProIleAlaLeuGlnArg 195
604 GACGATTCAAACGCGCCGATACAGCCCGA..... 638
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195 rgGlnArgHisGlyArgHisArgProAlaArgProAlaArgSerAlaGln 211
639 .....GCTGACAGATCGGCAATGCCG 661
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212 LysThrThrAlaArgThrProSerProAlaArgProIleAlaLeuGlnAr 228
662 CCGAAGCCTTCACGCGCACTGCAATTCGCAAAACATCATCGCGCG 711
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228 gArg.....GlnArgHisGlyArgHisArgHisGlyHisHisArgSerA 243
712 GCAGGGAATTTGTCGCGCAG.....CGATGCCGTGACAGGTAT 752
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243 IagIuLysThrThrAlaArgThrProSerProAlaArgProIleAlaLeu 259
753 AAGCGAGGCTCAACATCTGTCTCAT...GCACGCTTGGCTGCTTT 799
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260 GlnArgArgGlnArgHisGlyArgHisArgProAlaArgProIleAla 276
800 CCACCCAAACAGATGCGCGCATCAACGATTTGCAGATATGCG.... 845
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276 uGlnArgArg.....GlnArgHisGlyArgHisArgProAla 288
846 .....GCMACTCAAGACTATGCCGACGACGCGCATCGCGATG 884
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288 rgProtrilleAlaLeuGlnArg.....ArgGlnArgHisGlyArg... 301
885 GCGAGTCCAAACCCCAATGCCGACAGCATAGAGCCGTCAGAGATA 934
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302 HisArgProIleProIleAlaLeuGlnArgArgGlnArg..... 315
935 TCTTTATGGAGCCATCCCATCAAGAGATTGAGCTGCCGGGMAAA 984
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316 .....HisGlyArgHisArgProIleProIleThrLeuG 328
985 TACGCTTGGCGCGCAT.....CAGCGCACATCTGTCAAGCG 1022
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328 LnaArgThr**ArgHisArgCysHisArgHisGlyHisProLeuProLe 344
1023 GTGCGAGATGGCGCGCATCTGCGCAAGAGGAAATCCGCGCTCAGCG 1072
    :|||:|
344 u.GlnArgThr**GlnHisGlyCysHisArgProIleProIleAla 360
1073 ACAATTTTGGCGATCGGCATACGCAAAATACCGTCCCTTACATGCC 1122
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361 Leu.....GlnArgThr**ProAlaTrpThrProLeuAlaMet... 373
1123 CGAATATCCGTTCAAACTTGAGCAGCGCTTACGCAAGAAACATCAC 1172
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374 ....AlaThrHisArgSerThrLysLysIleThrAlaTrpThrProSer 389
1173 CTCTCAACCGTGGCGCGCTCAA 1195
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389 roArgProProIleAlaLeuGln 396
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